

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: February 14, 2003, 13:44:04 ; Search time 34 Seconds
(without alignments)
1412.029 Million cell updates/sec

Title: US-09-869-136-2
Perfect score: 1207
Sequence: 1 MKTKLIFSFTSIFALISR.....KDNKSFNIDKIGHLDIEIDS 233

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues 671580

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL21:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rviro:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1157	95.9	256	Q9SLH8	Q9slh8 streptococc
2	1126	93.3	233	Q99XW1	Q99xw1 streptococc
3	1091	90.4	209	Q9RQ55	Q9rq55 streptococc
4	1070	88.6	209	Q9LAD8	Q9lad8 streptococc
5	1069	88.6	209	Q9LAE0	Q9lae0 streptococc
6	1069	88.6	209	Q9LAC6	Q9lac6 streptococc
7	1069	88.6	209	Q9LAC5	Q9lac5 streptococc
8	1066	88.3	209	Q9LAE1	Q9lae1 streptococc
9	1063	88.1	256	Q9XR88	Q9xr88 streptococc
10	1062	88.0	209	Q9LAC4	Q9lac4 streptococc
11	1060	87.8	209	Q9LAD6	Q9lad6 streptococc
12	1059	87.7	209	Q9LAD2	Q9lad2 streptococc
13	1059	87.7	256	Q9SLH9	Q9slh9 streptococc
14	1058	87.7	209	Q9LAD1	Q9lad1 streptococc
15	1055	87.4	209	Q9LAC7	Q9lac7 streptococc
16	1054	87.3	209	Q9LAC9	Q9lac9 streptococc

17	1052	87.2	209	2	Q9LAC3	Q9lac3 streptococc
18	1046	86.7	209	2	Q9LAC8	Q9lac8 streptococc
19	1042	86.3	209	2	Q9LAD4	Q9lad4 streptococc
20	1038	85.2	209	2	Q9LAD7	Q9lad7 streptococc
21	1027	85.1	209	2	Q9LAD5	Q9lad5 streptococc
22	1027	85.1	209	2	Q9LAD3	Q9lad3 streptococc
23	1018	84.3	209	2	Q9LAD9	Q9lad9 streptococc
24	1015	84.1	209	2	Q9LAD0	Q9lad0 streptococc
25	310.5	25.7	256	2	Q9VLW7	Q9vwl7 staphylococ
26	309.5	25.6	242	2	Q93CC6	Q93cc6 staphylococ
27	308	25.5	240	16	Q9F0L7	Q9f0l7 staphylococ
28	300.5	24.9	242	2	Q54476	Q54476 staphylococ
29	297.5	24.6	242	16	Q85383	Q85383 staphylococ
30	295.5	24.5	242	2	Q93CC5	Q93cc5 staphylococ
31	283.5	23.5	218	2	Q8RR75	Q8rr75 staphylococ
32	276	22.9	239	2	Q9EZM7	Q9ezm7 staphylococ
33	274	22.7	239	16	Q99T47	Q99t47 staphylococ
34	262	21.7	206	2	Q34512	Q34512 streptococc
35	259	21.5	232	16	Q99QN1	Q99qn1 streptococc
36	251.5	20.8	260	16	Q931M4	Q931m4 staphylococ
37	240	19.9	210	2	Q9K2G9	Q9k2g9 staphylococ
38	238.5	19.8	225	2	Q8VVM1	Q8vwm1 streptococc
39	238.5	19.8	225	16	Q99Z21	Q99z21 streptococc
40	236.5	19.6	225	2	Q9L921	Q9l921 streptococc
41	232	19.2	234	2	Q93RR9	Q93rr9 streptococc
42	231.5	19.2	268	2	Q85217	Q85217 staphylococ
43	231	19.1	260	16	Q99SD3	Q99sd3 staphylococ
44	217.5	18.0	241	2	Q53585	Q53585 staphylococ
45	210.5	17.4	236	2	Q54696	Q54696 streptococc

ALIGNMENTS

RESULT 1

Q9SLH8 ID Q9SLH8; PRELIMINARY; PRT; 256 AA.
AC Q9SLH8;
DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DT 01-MAR-2002 (TRENBLrel. 20, Last annotation update)
DE SPEX protein precursor.
GN SPEX.
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillales;
OC Streptococcaceae; Streptococcus.
OX NCBI_TaxID=1314;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=12714 TYPE 12;
RX MEDLINE=20374978; PubMed=10913699;
RA Gerlach D., Fleischer B., Wagner M., Schmidt K.H., Vettermann S., Reichardt W.;
RT "Purification and Biochemical Characterization of a Basic Superantigen (SPEX/SMEZ3).";
RL FEMS Microbiol. Lett. 188:153-163(2000).
DR EMBL; AJ245405; CAB51744.1;
DR NSSP; P13163; 1SXT.
DR InterPro; IPR001361; Strep/Strep_Coxin.
DR Pfam; PF01123; Strep_Strep_Toxin; 1.
DR Pfam; PF02876; Strep_Strep_Tox_C; 1.
DR PRINTS; PR00279; BACTRLTOXIN.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
KW SIGNAL.
FT SIGNAL.
SQ SEQUENCE 256 AA; 29706 MW; 873D0BAFBE6DC332 CRC64;

Query Match 95.9%; Score 1157; DB 2; Length 256;
Best Local Similarity 97.0%; Pred. No. 1.6e-77;
Matches 226; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
QY 1 MKTKLIFSFTSIFALISRPFVGLVDNNSLLRNYSIVVEYSDIVDFKTSNHLVTK 60
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Db 24 MKTKLIFSFTSIFAIISRPVGLVNDNLSLNSTIVYEYSDIVDFKSHNLVTK 83
QY 61 KLDVRDARDFINSEMEYAAANDFKTGDKIAVESVPDWNLYLSKGVYATYTGITPYQK 120
DB 84 KLDVRDARDFINSEMEYAAANDFKTGDKIAVESVPDWNLYLSKGVYATYTGITPYQK 143
QY 121 TSIPKNTPVNLWNGKQISVPYNEISNTKTTVTAQIEDLKVRFELIAHQHLYSGSSYKS 180
DB 144 LOYKISLWNLWNGKQISVPYNEISNTKTTVTAQIEDLKVRFELIAHQHLYSGSSYKS 203
QY 181 GRLVFHTNDSKYSFDFLVGVYRDKESIFKVKYKDNKSFNIDKIGHLDIEIDS 233
DB 204 GRLVFHTNDSKYSFDFLVGVYRDKESIFKVKYKDNKSFNIDKIGHLDIEIDS 256

RESULT 2
Q99XW1
ID Q99XW1 PRELIMINARY; PRT; 233 AA.
AC Q99XW1;
DT 01-JUN-2001 (TReMBLrel. 17, Created)
DT 01-JUN-2001 (TReMBLrel. 17, Last sequence update)
DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
DE Mitogenic exotoxin 2.
GN SMEZ OR SPI1998.
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillales;
OC Streptococcaceae; Streptococcus.
OX NCBI_TaxID=1314;
RN [1]
RN SEQUENCE FROM N.A.
RC STRAIN=3F390 / ATCC 700294 / SEROTYPE M1;
RX MEDLINE=21192684; PubMed=1175796;
RA Ferratti J.J., McShan W.M., Ajdic D.J., Savic D.J., Lyon K.,
Primeaux C., Szatec S., Suvorov A.N., Kanton S., Lai H.S., Lin S.P.,
Yuan Y., Jia H.G., Najjar F.Z., Ren Q., Zhi H., Song L., White J.,
Yuan X., Clifton S.W., Roe B.A., McLaughlin R.,
*Complete genome sequence of an M1 strain of Streptococcus pyogenes.*;
Proc. Natl. Acad. Sci. U.S.A. 98:4658-4663(2001).
RL ENBL; AF006622; AAK34680.1; -.
DR HSSP; P13163; ISXT.
DR InterPro: IPR001961; Strep/Strep-toxin.
DR Pfam; PF01123; Strep_strip_toxin; 1.
DR Pfam; PF02876; Strep_strip_toxin_C; 1.
DR PRINTS; PR00279; BACTRLTOXIN.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
KW Complete proteome.
SQ SEQUENCE 233 AA; 27032 MW; E9A8C3811ECA01F9 CRC64;

Query Match 93.3%; Score 1126; DB 16; Length 233;
Best Local Similarity 92.7%; Pred. No. 2.7e-75;
Matches 216; Conservative 8; Mismatches 9; Indels 0; Gaps 0;

QY 1 MKTKLIFSFTSIFAIISRPVGLVNDNLSLNSTIVYEYSDIVDFKSHNLVTK 60
DB 1 MKTKLIFSFTSIFAIISRPVGLVNDNLSLNSTIVYEYSDIVDFKSHNLVTK 60
QY 61 KLDVRDARDFINSEMEYAAANDFKTGDKIAVESVPDWNLYLSKGVYATYTGITPYQK 120
DB 61 KLDVRDARDFINSEMEYAAANDFKTGDKIAVESVPDWNLYLSKGVYATYTGITPYQK 120
QY 121 TSIPKNTPVNLWNGKQISVPYNEISNTKTTVTAQIEDLKVRFELIAHQHLYSGSSYKS 180
DB 121 EPMKSNIPVNLWNRQIPVYNIQISTNKTITVTAQIEDLKVRFELISQHLYSGSSYKS 180
QY 181 GRLVFHTNDSKYSFDFLVGVYRDKESIFKVKYKDNKSFNIDKIGHLDIEIDS 233
DB 181 GLVLFHTNDSKYSFDFLVGVYRDKESIFKVKYKDNKSFNIDKIGHLDIEIDS 233

RESULT 3
Q9RQ05
ID Q9RQ05 PRELIMINARY; PRT; 209 AA.
AC Q9RQ05;

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DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-MAR-2002 (TReMBLrel. 20, Last annotation update)
DE Mitogenic exotoxin 2 (Fragment).
GN SMEZ-2.
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillales;
OC Streptococcaceae; Streptococcus.
OX NCBI_TaxID=1314;
RN [1]
RN SEQUENCE FROM N.A.
RC STRAIN=2035;
RX MEDLINE=99093428; PubMed=9874566;
RA Profit T., Moffatt S.L., Berkahn C.J., Fraser J.D.;
*Identification and characterization of novel superantigens from
Streptococcus pyogenes.*;
J. Exp. Med. 189:89-102(1999).
RL ENBL; AF086626; AAD52087.1; -.
DR HSSP; P13163; ISXT.
DR InterPro: IPR001961; Strep/Strep-toxin.
DR Pfam; PF01123; Strep_strip_toxin; 1.
DR Pfam; PF02876; Strep_strip_toxin_C; 1.
DR PRINTS; PR00279; BACTRLTOXIN.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
FT NON_TER 1
SQ SEQUENCE 209 AA; 24131 MW; 52BF7911BB100152 CRC64;

Query Match 90.4%; Score 1091; DB 2; Length 209;
Best Local Similarity 100.0%; Pred. No. 8.8e-73;
Matches 209; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 25 LEVDNNSLLRNISTIVYEYSDIVDFKSHNLVTKKLDVRDARDFINSEMEYAAANDF 84
DB 1 LEVDNNSLLRNISTIVYEYSDIVDFKSHNLVTKKLDVRDARDFINSEMEYAAANDF 60
QY 85 KTGDKTAVFVSPDWNLYLSKGVYATYTGITPYQKTSIPKNTPVNLWNGKQISVPYNE 144
DB 61 KTGDKTAVFVSPDWNLYLSKGVYATYTGITPYQKTSIPKNTPVNLWNGKQISVPYNE 120
QY 145 ISTNKTITVTAQIEDLKVRFELIAHQHLYSGSSYKSGLVFTHTNDSKYSFDFLVYGYR 204
DB 121 ISTNKTITVTAQIEDLKVRFELIAHQHLYSGSSYKSGLVFTHTNDSKYSFDFLVYGYR 180
QY 205 DKESIFKVKYKDNKSFNIDKIGHLDIEIDS 233
DB 181 DKESIFKVKYKDNKSFNIDKIGHLDIEIDS 209

RESULT 4
Q9LAD8
ID Q9LAD8 PRELIMINARY; PRT; 209 AA.
AC Q9LAD8;
DT 01-OCT-2000 (TReMBLrel. 15, Created)
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
DT 01-MAR-2002 (TReMBLrel. 20, Last annotation update)
DE Mitogenic exotoxin 2-7 (Fragment).
GN SMEZ-7.
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillales;
OC Streptococcaceae; Streptococcus.
OX NCBI_TaxID=1314;
RN [1]
RN SEQUENCE FROM N.A.
RC STRAIN=11574;
RX MEDLINE=20733982; PubMed=10811869;
RA Profit T., Moffatt S.L., Weller K.D., Paterson A., Martin D.,
Fraser J.D.;
*The Streptococcal Superantigen SMEZ Exhibits Wide Allelic Variation,
Mosaic Structure, and Significant Antigenic Variation.*;
J. Exp. Med. 191:1765-1776(2000).
RL ENBL; AF143657; AAF66657.1; -.
DR HSSP; P13163; ISXT.
DR InterPro: IPR001961; Strep/Strep-toxin.

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DR	Pfam; PF01123; Stap_Strp_toxin; 1.
DR	Prints; PF02876; Stap_Strp_tox_C; 1.
DR	PRINTS; PR00279; BACTRLTOXIN.
DR	PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
FT	NON_TER 1
SQ	SEQUENCE 209 AA; 24064 MW; 67E977CD5AA934F7 CRC64;
 Query Match 88.6%; Score 1070; DB 2; Length 209; Best Local Similarity 97.6%; Pred. No. 3.1e-71; Matches 204; Conservative 2; Mismatches 3; Indels 0; Gaps	
QY	25 LEVDNNSLLRNISTIVIEYSDIVIDFKTSHNLVTKKLDVRDARDFINSEMDHYAANDF 84
Dd	1 LEVDNNSLLRNISTIVIEYSDIVIDFKTSHNLVTKKLDVRDARDFINSEMDHYAANDF 60
QY	85 KTGDKIAVFSVPDDWNYLSKGKVTAITYGGITPYOKTSIPKNIPVNWLINGKOISVPYNE 144
Dd	61 KAGDKIAVFSVPDDWNYLSEGKVTAITYGGITPYOKTSIPKNIPVNWLINGKOISVPYNE 120
QY	145 ISTNKTTVTVAQEIDLKYRKFLIAHQHLYSSGSSYKSGRLVFHTNDNSKYSDFLFVGVYR 204
Dd	121 ISTNKTTVTVAQEIDLKYRKFLIAHQHLYSSGSSYKSGKLVEHTNDNSKYSDFLFVGVYR 180
QY	205 DKESIFKVKYKDKNFSNIDKIGHLDIIDS 233
Dd	181 DKESIFKVKYKDKNFSNIDKIGHLDIIDS 209
 RESULT 5 PRELIMINARY; PRT; 209 AA. O9LAEO O9LAEO ID AC AC O9LAEO DT 01-OCT-2000 (TrEMBLrel. 15, Created) DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update) DE 01-MAR-2002 (TrEMBLrel. 20, Last annotation update) DE Mitogenic exotoxin Z-4 (Fragment). GN SMEZ-4. OC Streptococcus pyogenes. OC Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillales; OX Streptococcaceae; Streptococcus. NCBI_TaxId=1314; RN [1] RC SEQUENCE FROM N.A. RP STRAIN=7683; RX MEDLINE=20373982; PubMed=108111869; RA Prof T., Moffatt S.L., Weller K.D., Paterson A., Martin D., EA Fraser J.D.; FA "The Streptococcal Superantigen SPEZ Exhibits Wide Allelic Variation, NT Mosaic Structure, and Significant Antigenic Variation."; RR J. Exp. Med. 191:1765-1776(2000). RR EMBL; AF143654; AAF66655.1; - DR HSP; P13163; LSXT. DR InterPro; IPR001961; Staph/Strep_toxin. DR Pfam; PF01123; Stap_Strp_toxin; 1. DR Pfam; PF02876; Stap_Strp_tox_C; 1. DR PRINTS; PR00279; BACTRLTOXIN. DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1. FT NON_TER 1 SQ SEQUENCE 209 AA; 24108 MW; 67EC279BBC4A8247 CRC64;	
 Query Match 88.6%; Score 1069; DB 2; Length 209; Best Local Similarity 97.6%; Pred. No. 3.7e-71; Matches 204; Conservative 2; Mismatches 3; Indels 0; Gaps	
QY	25 LEVDNNSLLRNISTIVIEYSDIVIDFKTSHNLVTKKLDVRDARDFINSEMDHYAANDF 84
Dd	1 LEVDNNSLLRNISTIVIEYSDIVIDFKTSHNLVTKKLDVRDARDFINSEMDHYAANDF 60
QY	85 KTGDKIAVFSVPDDWNYLSKGKVTAITYGGITPYOKTSIPKNIPVNWLINGKOISVPYNE 144
Dd	61 KOGDKIAVFSVPDDWNYLSEGKVTAITYGGITPYOKTSIPKNIPVNWLINGKOISVPYNE 120
QY	145 ISTNKTTVTVAQEIDLKYRKFLIAHQHLYSSGSSYKSGRLVFHTNDNSKYSDFLFVGVYR 204

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OX NCBI_TaxID=1314;
RN SEQUENCE FROM N.A.
RP STRAIN=11222;
RX MEDLINE=20273982; PubMed=10811869;
RA Proft T., Mofatt S.L., Weller K.D., Paterson A., Martin D.,
RA Fraser J.D.;
RT "The Streptococcal Superantigen SMEZ Exhibits Wide Allelic Variation,
RL Mosaic Structure, and Significant Antigenic Variation.";
RL J. Exp. Med. 191:1765-1776(2000).
DR EMBL: AF143671; AAF66670.1; -.
DR HSSP: P13163; 1SXT.
DR InterPro: IPR001961; Strep_toxin.
DR Pfam: PF01123; Strep_toxin; 1.
DR Pfam: PF02876; Strep_toxin; 1.
DR PRINTS: PR00279; BACTRLTOXIN.
DR PROSITE: PS00278; STAPH_STREP_TOXIN_2; 1.
FT NON_TER
SQ SEQUENCE 209 AA; 24106 MW; 67FD2696FA4BC55A CRC64;

Query Match 88.6%; Score 1069; DB 2; Length 209;
Best Local Similarity 97.6%; Pred. No. 3.7e-71;
Matches 204; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 25 LEVDNNSLLRNISTIVYEYSDIVDFKTSNHLVTKKLDVDRDARDFINSEMEYAAANDF 84
Db 1 LEVDNNSLLRNISTIVYEYSDIVDFKTSNHLVTKKLDVDRDARDFINSEMEYAAANDF 60
QY 85 KTGDKIAVSPFDWNLKSGKVTAYTYGGITPYQKTSIPKNIPVNLWNGKQISVPYNE 144
Db 61 KTGDKIAVSPFDWNLSEGVIAVYTYGGITPYQKTSIPKNIPVNLWNGKQISVPYNE 120
QY 145 ISTNKTVTVAQETDLKVRFLTAHQHLYSSGSSYKSGRLVFHTNDNSDKYSFDFLYVGYR 204
Db 121 ISTNKTVTVAQETDLKVRFLTAHQHLYSSGSSYKSGRLVFHTNDNSDKYSFDFLYVGYR 180
QY 205 DKESIFKVKYKDNKSFNIDKIGHLDIEIDS 233
Db 181 DKESIFKVKYKDNKSFNIDKIGHLDIEIDS 209

Query Match 88.6%; Score 1069; DB 2; Length 209;
Best Local Similarity 97.6%; Pred. No. 3.7e-71;
Matches 204; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 25 LEVDNNSLLRNISTIVYEYSDIVDFKTSNHLVTKKLDVDRDARDFINSEMEYAAANDF 84
Db 1 LEVDNNSLLRNISTIVYEYSDIVDFKTSNHLVTKKLDVDRDARDFINSEMEYAAANDF 60
QY 85 KTGDKIAVSPFDWNLKSGKVTAYTYGGITPYQKTSIPKNIPVNLWNGKQISVPYNE 144
Db 61 KTGDKIAVSPFDWNLSEGVIAVYTYGGITPYQKTSIPKNIPVNLWNGKQISVPYNE 120
QY 145 ISTNKTVTVAQETDLKVRFLTAHQHLYSSGSSYKSGRLVFHTNDNSDKYSFDFLYVGYR 204
Db 121 ISTNKTVTVAQETDLKVRFLTAHQHLYSSGSSYKSGRLVFHTNDNSDKYSFDFLYVGYR 180
QY 205 DKESIFKVKYKDNKSFNIDKIGHLDIEIDS 233
Db 181 DKESIFKVKYKDNKSFNIDKIGHLDIEIDS 209

Query Match 88.1%; Score 1063; DB 2; Length 256;
Best Local Similarity 89.7%; Pred. No. 1.3e-70;
Matches 209; Conservative 5; Mismatches 19; Indels 0; Gaps 0;

QY 1 MKKTKLIFSFTSIFTAISRPFVGLVDNNSLLRNISTIVYEYSDIVDFKTSNHLVTK 60
Db 24 MKKTKLIFSFTSIFTAISRPFVGLVDNNSLLRNISTIVYEYSDIVDFKTSNHLVTK 83
QY 61 KLDVDRDARDFINSEMEYAAANDFKTGKIAVSPFDWNLKSGKVTAYTYGGITPYQK 120
Db 84 KLDVDRDARDFINSEMEYAAANDFKTGKIAVSPFDWNLKSGKVTAYTYGGITPYQK 143
QY 121 TSIPKNIPVNLWNGKQISVPYNEISTNKTVTVAQETDLKVRFLTAHQHLYSSGSSYKS 180
Db 144 LQYKLSLVYIGINRKQIPVYNQISPTKTTVAQETDLKVRFLTAHQHLYSSGSSYKS 203
QY 181 GRLVFHTNDNSDKYSFDFLYVGYRDKESIFKVKYKDNKSFNIDKIGHLDIEIDS 233
Db 204 GKLVTHTNDNSDKYSFDFLYVGYRDKESIFKVKYKDNKSFNIDKIGHLDIEIDS 256
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OX NCBI_TaxID=1314;
RN SEQUENCE FROM N.A.
RP STRAIN=11222;
RX MEDLINE=20273982; PubMed=10811869;
RA Proft T., Mofatt S.L., Weller K.D., Paterson A., Martin D.,
RA Fraser J.D.;
RT "The Streptococcal Superantigen SMEZ Exhibits Wide Allelic Variation,
RL Mosaic Structure, and Significant Antigenic Variation.";
RL J. Exp. Med. 191:1765-1776(2000).
DR EMBL: AF143671; AAF66670.1; -.
DR HSSP: P13163; 1SXT.
DR InterPro: IPR001961; Strep_toxin.
DR Pfam: PF01123; Strep_toxin; 1.
DR Pfam: PF02876; Strep_toxin; 1.
DR PRINTS: PR00279; BACTRLTOXIN.
DR PROSITE: PS00278; STAPH_STREP_TOXIN_2; 1.
FT NON_TER
SQ SEQUENCE 209 AA; 24106 MW; 67FD2696FA4BC55A CRC64;

Query Match 88.3%; Score 1066; DB 2; Length 209;
Best Local Similarity 97.1%; Pred. No. 6.1e-71;
Matches 203; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 25 LEVDNNSLLRNISTIVYEYSDIVDFKTSNHLVTKKLDVDRDARDFINSEMEYAAANDF 84
Db 1 LEVDNNSLLRNISTIVYEYSDIVDFKTSNHLVTKKLDVDRDARDFINSEMEYAAANDF 60
QY 85 KTGDKIAVSPFDWNLKSGKVTAYTYGGITPYQKTSIPKNIPVNLWNGKQISVPYNE 144
Db 61 KAGDKIAVSPFDWNLKSGRVTAYTYGGITPYQKTSIPKNIPVNLWNGKQISVPYNE 120
QY 145 ISTNKTVTVAQETDLKVRFLTAHQHLYSSGSSYKSGRLVFHTNDNSDKYSFDFLYVGYR 204
Db 121 ISTNKTVTVAQETDLKVRFLTAHQHLYSSGSSYKSGRLVFHTNDNSDKYSFDFLYVGYR 180
QY 205 DKESIFKVKYKDNKSFNIDKIGHLDIEIDS 233
Db 181 DKESIFKVKYKDNKSFNIDKIGHLDIEIDS 209

Query Match 88.1%; Score 1063; DB 2; Length 256;
Best Local Similarity 89.7%; Pred. No. 1.3e-70;
Matches 209; Conservative 5; Mismatches 19; Indels 0; Gaps 0;

QY 1 MKKTKLIFSFTSIFTAISRPFVGLVDNNSLLRNISTIVYEYSDIVDFKTSNHLVTK 60
Db 24 MKKTKLIFSFTSIFTAISRPFVGLVDNNSLLRNISTIVYEYSDIVDFKTSNHLVTK 83
QY 61 KLDVDRDARDFINSEMEYAAANDFKTGKIAVSPFDWNLKSGKVTAYTYGGITPYQK 120
Db 84 KLDVDRDARDFINSEMEYAAANDFKTGKIAVSPFDWNLKSGKVTAYTYGGITPYQK 143
QY 121 TSIPKNIPVNLWNGKQISVPYNEISTNKTVTVAQETDLKVRFLTAHQHLYSSGSSYKS 180
Db 144 LQYKLSLVYIGINRKQIPVYNQISPTKTTVAQETDLKVRFLTAHQHLYSSGSSYKS 203
QY 181 GRLVFHTNDNSDKYSFDFLYVGYRDKESIFKVKYKDNKSFNIDKIGHLDIEIDS 233
Db 204 GKLVTHTNDNSDKYSFDFLYVGYRDKESIFKVKYKDNKSFNIDKIGHLDIEIDS 256
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QY 85 KTGDKIAVSPFDWNYLSKGVTAATYGGITPYQKTSIPKNIPVNLWINGKQISVPYNE 144
 DB 61 KAGDKIAVSPFDWNYLSKGVTAATYGGITPYQKTSIPKNIPVNLWINGKQISVPYNE 120
 QY 145 ISTNKTVTAAQEDILKVRKFLIAHQHLYSSGSSYKSRGLVFHTNDNSDKYSFDFLYVGYR 204
 DB 121 ISTNKTVTAAQEDILKVRKFLIAHQHLYSSGSSYKSKGLVFHTNDNSDKYSFDFLYVGYR 180
 QY 205 DKESIFKVKDKNSFNIDKIGHLDIEIDS 233
 DB 181 DKESIFKVKDKNSFNIDKIGHLDIEIDS 209

RESULT 13
 Q9SLH9 PRELIMINARY; PRT; 256 AA.
 AC Q9SLH9;
 DT 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
 DE SPEG-1 protein precursor.
 GN SPEG.
 OS Streptococcus pyogenes.
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillales;
 OC Streptococcaceae; Streptococcus.
 OX NCBI_TaxID=1314;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=27195;
 RX MEDLINE=20374978; PubMed=10913699;
 RA Gerlach D., Fleischer B., Wagner M., Schmidt K.H., Vettermann S.,
 RA Reichardt W.;
 RT "Purification and Biochemical Characterization of a Basic Superantigen
 RT (SPEG/SMEZ3)". Lett. 188:153-163(2000).
 RL PEMS Microbiol.
 DR EMBL; AJ243890; CAB51142.1;
 DR HSSP; P13380; LAN8.
 DR InterPro; IPR001961; Strep/Strep-toxin.
 DR Pfam; PF01123; Strep_Strp_toxin; 1.
 DR Pfam; PF02876; Strep_Strp_tox_C; 1.
 DR PRINTS; PR00279; BACTRLTOXIN.
 DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
 KW Signal.
 FT SIGNAL
 SQ SEQUENCE 256 AA; 29610 MW; 149E1774D0D04FC7 CRC64;

Query Match 87.7%; Score 1059; DB 2; Length 256;
 Best Local Similarity 89.3%; Pred. No. 2.5e-70;
 Matches 208; Conservative 5; Mismatches 20; Indels 0; Gaps 0;

QY 1 MKTKLIFGTSIFIAISRPFGLVDNNSLLRNITVVEYSDIVDFKTSNHLVTK 60
 DB 24 MKTKLIFGTSIFIAISRPFGLVDNNSLLRNITVVEYSDIVDFKTSNHLVTK 83
 QY 61 KLDVRDARDFINSEMDYANDFKTGDKIAVSPFDWNYLSKGVTAATYGGITPYQK 120
 DB 84 KLDVRDARDFINSEMDYANDFKTGDKIAVSPFDWNYLSKGVTAATYGGITPYQK 143
 QY 121 TSIPKNIPVNLWINGKQISVPYNEISTNKTVTAAQEDILKVRKFLIAHQHLYSSGSSYKS 180
 DB 144 LOYLKISLVIYGINRKQIPVNPYQISPTKTTVTAQEDILKVRKFLISQHLYSGSSYKS 203
 QY 181 GRLVHTNDNSDKYSFDFLYVGYRDKESIFKVKDKNSFNIDKIGHLDIEIDS 233
 DB 204 GKLVHTNDNSDKYSFDFLYVGYRDKESIFKVKDKNSFNIDKIGHLDIEIDS 256

RESULT 14
 Q9LAD1 PRELIMINARY; PRT; 209 AA.
 AC Q9LAD1;
 DT 01-OCT-2000 (TREMBlrel. 15, Created)

DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
 DE Mitogenic exotoxin Z-14 (Fragment).
 GN SMEZ-14.
 OS Streptococcus pyogenes.
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillales;
 OC Streptococcaceae; Streptococcus.
 OX NCBI_TaxID=1314;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=4202;
 RX MEDLINE=20273982; PubMed=10811869;
 RA Proft T., Moffatt S.L., Weller K.D., Paterson A., Martin D.,
 RA Fraser J.D.;
 RT "The Streptococcal Superantigen SMEZ Exhibits Wide Allelic Variation,
 RT Mosaic Structure, and Significant Antigenic Variation.";
 RL J. Exp. Med. 191:1765-1776(2000).
 DR EMBL; AF143664; AAF66664.1;
 DR HSSP; P13163; 1SXT.
 DR InterPro; IPR001961; Strep/Strep-toxin.
 DR Pfam; PF01123; Strep_Strp_toxin; 1.
 DR Pfam; PF02876; Strep_Strp_tox_C; 1.
 DR PRINTS; PR00279; BACTRLTOXIN.
 DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
 FT NON_TER
 SQ SEQUENCE 209 AA; 24122 MW; 0CF5D429E1B968FE CRC64;

Query Match 87.7%; Score 1058; DB 2; Length 209;
 Best Local Similarity 96.2%; Pred. No. 2.3e-70;
 Matches 201; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 25 LEVDNNSLLRNITVVEYSDIVDFKTSNHLVTKKLDVRDARDFINSEMDYANDF 84
 DB 1 LEVDNNSLLRNITVVEYSDIVDFKTSNHLVTKKLDVRDARDFINSEMDYANDF 60
 QY 85 KTGDKIAVSPFDWNYLSKGVTAATYGGITPYQKTSIPKNIPVNLWINGKQISVPYNE 144
 DB 61 KAGDKIAVSPFDWNYLSKGVTAATYGGITPYQKTSIPKNIPVNLWINGKQISVPYNE 120
 QY 145 ISTNKTVTAAQEDILKVRKFLIAHQHLYSSGSSYKSRGLVFHTNDNSDKYSFDFLYVGYR 204
 DB 121 ISTNKTVTAAQEDILKVRKFLIAHQHLYSSGSSYKSKGLVFHTNDNSDKYSFDFLYVGYR 180
 QY 205 DKESIFKVKDKNSFNIDKIGHLDIEIDS 233
 DB 181 DKESIFKVKDKNSFNIDKIGHLDIEIDS 209

RESULT 15
 Q9LAC7 PRELIMINARY; PRT; 209 AA.
 AC Q9LAC7;
 DT 01-OCT-2000 (TREMBlrel. 15, Created)
 DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
 DE Mitogenic exotoxin Z-18 (Fragment).
 GN SMEZ-18.
 OS Streptococcus pyogenes.
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillales;
 OC Streptococcaceae; Streptococcus.
 OX NCBI_TaxID=1314;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=10763;
 RX MEDLINE=20273982; PubMed=10811869;
 RA Proft T., Moffatt S.L., Weller K.D., Paterson A., Martin D.,
 RA Fraser J.D.;
 RT "The Streptococcal Superantigen SMEZ Exhibits Wide Allelic Variation,
 RT Mosaic Structure, and Significant Antigenic Variation.";
 RL J. Exp. Med. 191:1765-1776(2000).
 DR EMBL; AF143668; AAF66668.1;
 DR HSSP; P13163; 1SXT.
 DR InterPro; IPR001961; Strep/Strep-toxin.

DR Pfam: PF01123; Staph_Strp_toxin; 1.
 DR Pfam: PF02876; Staph_Strp_tox_C; 1.
 DR PRINTS: PR00279; BACTRLTOXIN.
 DR PROSITE: PS00278; STAPH_STREP_TOXIN_2; 1.
 FT NON_TER 1
 SQ SEQUENCE 209 AA; 24214 MW; 5755ED7340D77527 CRC64;

Query Match 87.4%; Score 1055; DB 2; Length 209;
 Best Local Similarity 96.2%; Pred.No. 3.9e-70;
 Matches 201; Conservative 4; Mismatches 4; Indels 0; Gaps 0;
 QY 25 LEVDNNSLLRNLYSTIVYEYSDIVIOFKTSHNLVTKKLDVDRDARDFINSEMDEYAANDF 84
 Db 1 LEVDNNSLLRNLYSTIVYEYSDIVIOFKTSHNLVTKKLDVDRDARDFINSEMDEYAANDF 60
 QY 85 KTGDKIAVFSVPFDWNYLSKGVKVTAYTYGGITPYQKTSIPKNIPVNLWINGKQISVPYNE 144
 Db 61 KTGDKIAVFSVPFDWNYLSKGVKVTAYTYGGITPYQKTSIPKNIPVNLWINGKQISVPYNE 120
 QY 145 ISTNKTVTVAQIDILKVRFLIAQHOLYSSGSSYKSGRLVFHTNDNSDKYSFDLFYVGYR 204
 Db 121 ISTNKTVTVAQIDILKVRFLIAQHOLYSSGSSYKSGRLVFHTNDNSDKYSFDLFYVGYR 180
 QY 205 DKESIFKYKDNKSNIDKIGHLDIEIDS 233
 Db 181 DKESIFKYKDNKSNIDKIGHLDIEIDS 209

Search completed: February 14, 2003, 13:45:47
 Job time : 36 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: February 14, 2003, 13:44:09 ; Search time 20 seconds
(without alignments)
1119.966 Million cell updates/sec

Title: US-09-869-136-2

Perfect score: 1207
Sequence: 1 MKTKLIFSFTSIFIAISR.....KDKSFNIDKIGHLDIEIDS 233

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

PIR73:*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	308	25.5	240	2 G89991	extracellular ente
2	297.5	24.6	242	2 C89969	extracellular ente
3	296	24.5	235	2 A30509	exotoxin C precurs
4	274	22.7	239	2 D89969	enterotoxin SEM [i
5	258.5	21.4	257	2 A28179	enterotoxin E prec
6	251.5	20.8	257	2 A28664	enterotoxin A prec
7	251	20.8	258	2 A33953	enterotoxin D prec
8	231	19.1	260	2 C89984	enterotoxin P [imp
9	210.5	17.4	236	2 S18789	exotoxin A precurs
10	199.5	16.5	236	2 S18786	exotoxin type A pr
11	196.5	16.3	236	2 S18783	exotoxin type A pr
12	195.5	16.2	251	1 S29559	exotoxin type A pr
13	194.5	16.1	260	2 C89969	enterotoxin type A pr
14	165.5	13.7	238	2 H89968	enterotoxin Sen [i
15	162.5	13.5	266	1 ENSAB6	enterotoxin B prec
16	161	13.3	258	2 G89968	extracellular ente
17	158	13.1	266	2 A60114	enterotoxin C-2 pr
18	156	12.9	266	2 S11885	enterotoxin C3 - S
19	153.5	12.7	286	1 ENSAC1	enterotoxin C-1 pr
20	132.5	11.0	136	2 A89969	enterotoxin YENT2
21	122	10.1	250	1 A26152	streptococcal pyro
22	119	9.9	231	2 D89807	exotoxin 11 [impor
23	118.5	9.8	292	2 B89807	exotoxin 9 [impor
24	116.5	9.7	356	2 A89807	exotoxin 8 [impor
25	113.5	9.4	234	2 B89992	toxic shock syndro
26	113	9.4	232	2 F89807	exotoxin 13 [impor
27	112.5	9.3	234	1 XCSAS1	toxic shock syndro
28	110.5	9.2	4688	2 F82885	hypothetical prote
29	106.5	8.8	464	2 S44603	C02F5.1 protein -

30 106.5 8.8 594 2 A82913
31 104.5 8.7 241 2 B89888
32 1216 8.5 1216 2 F84773
33 102.5 8.5 626 2 E82273
34 102 8.5 227 2 G89807
35 102 8.5 540 2 T20352
36 102 8.5 963 2 C90535
37 100.5 8.3 532 2 G84931
38 100.5 8.3 616 2 B90554
39 100.5 8.3 631 2 C90552
40 99.5 8.2 544 2 B81290
41 99 8.2 971 2 C82880
42 98.5 8.2 496 2 A81340
43 98 8.1 1061 2 H90084
44 97.5 8.1 226 2 G89806
45 97.5 8.1 860 2 T28227

ALIGNMENTS

RESULT 1

G89991
extracellular enterotoxin L [imported] - Staphylococcus aureus (strain N315)
C:Species: Staphylococcus aureus
C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001
C:Accession: G89991
R:Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.;
ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu,
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A:Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.
A:Reference number: A89758; MUID:21311952; PMID:11418146
A:Accession: G89991
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-240 <KUR>
A:Cross-references: GB:BA000018; PID:g13701803; PIDN:BA843096.1; GSPDB:GN00149
A:Experimental source: strain N315
C:Genetics:
A:Gene: sel
C:Superfamily: enterotoxin B

Query Match 25.5%; Score 308; DB 2; Length 240;
Best Local Similarity 33.5%; Pred. No. 1.5e-16;
Matches 83; Conservative 41; Mismatches 96; Indels 28; Gaps 8;
QY 1 MKTKLIFSFTSIFIAISRVPVGLVDNNSLLRNIYTVVEYSDIVDFKTSNHLVTK 60
DB 1 MKKRLLFVITLFTFSSNHTVLSNGDVGPNLRFYTK--YEYVNLK-NVKDKNSPESH 57
QY 61 KLDVRDARDFFINSEMDVYANDFKTGDKIAVSPFDNNYLSKGVTAITYGGITPYQ- 119
DB 58 RLEYSYKNDTLVAEPDNEYITSDLK-GKNVDVFGIYKY----GSNRTYIGGVTKAEN 111
QY 120 -KTSIPKNIPVNLWNGKQISVYNEISTNKTTPVTAQIDLRKVRFLAQHQLYSSG--- 175
DB 112 NKLDSPRIIPINLIINGKHQVTTKSVSTDKKMTVAQIDVYKRLYLDENIYGHNDTG 171
QY 176 -----SSYKSRRLVPHNNDNSDKYSFDLFYVGVYRDKESIFKVKDKNKSFNDR 223
DB 172 KGKEYGTSKRYSGFDKGSVVFMNDGSN-FSYDLFTYGYGLPESFLKIYKDNKTVDSQ 230
QY 224 IGHLDIEI 231
DB 231 F-HLDVEI 237

RESULT 2

C89969
extracellular enterotoxin type I precursor [imported] - Staphylococcus aureus (stra
C:Species: Staphylococcus aureus
C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001

C>Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 15-Oct-1999
C/Accession: A28179
R/Couch, J.L.; Soltis, M.T.; Betley, M.J.
J. Bacteriol. 170, 2954-2960, 1988
A/Title: Cloning and nucleotide sequence of the type E staphylococcal enterotoxin A
A/Reference number: A28179; M01D:88257005; PMID:3384800
A/Accession: A28179
A/Molecule type: DNA
A/Residues: 1-257 <COU>
A/Cross-references: GB:M21319; NID:g153001; PIDN:AAA26617.1; PID:g153002
C:Superfamily: enterotoxin B

```

Query Match      21.4%; Score 258.5; DB 2; Length 257;
Best Local Similarity 26.4%; Pred. No. 1e-12;
Matches 75; Conservative 55; Mismatches 67; Indels 87; Gaps 13;

QY 1 MKKPKLIFSFTSIIA--IISRPVFG-----LEVDNNSL--LRNIY--- 37
    |||| | :||| : | : :||| :||| :||| :||| :||| :||| :|||
Db 1 MKKTAFIL--LLFIALTLTSPLVNGSEKEINEKDRLRKSELQRNALSNLRQIYYN 57
    :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
QY 38 -----STIIVE-----YSDIVIDEKTSHNLVTKLDVRDARDFIN 73
    :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 58 EKATENKESDDQFLENTLLFKGFTGHVPYNLLVD-----LGSKDATNKYKG 106
    :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
QY 74 SEMDEYAANDFKTGDKIAVESVPEDWNYLSKG---KYTAYTYGGITPYOKTISI--PKNIP 128
    :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 107 KKVDLYCAY-----YGYQCAGGTPNKTCACMYGGVTLLHDNNRLTEEEKVP 150
    :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
QY 129 VNLWINKGQISVPYNEISTNNKTTVTAQEIDLKVKRFIAQHQLYSS---GSSYKSGRLVF 185
    :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 151 INLWDIGKQTTPIDKVKTSKEVTVQELDLQARHYLHGREGFLNSDSFGKGVGQGLIVF 210
    :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
QY 186 HTNDNSDKYSFDLFYGVYRKRKESIFKYVKONKSFNIDKIGHLDI 229
    :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 211 HSSSGS--TVSYDYFDAOGQYPDTLLRYTRDNKTNINSENL-HIDL 252
    :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||

```

RESULT 6
A28664
enterotoxin A precursor - Staphylococcus aureus
C:Species: Staphylococcus aureus
C>Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 15-Oct-1999
C:Accession: A28664; A29566
R:Betley, M.J.; Mekalanos, J.J.
J. Bacteriol. 170, 34-41, 1988
A:Title: Nucleotide sequence of the type A staphylococcal enterotoxin gene.
A:Reference number: A28664; MUID:89086892; PMID:3335483
A:Accession: A28664
A:Molecule type: DNA
A:Residues: 1-257 <BET>
A:Cross-References: GB:M18970; NID:g153120; PIDN:AAA26681.1; PID:g153121
A:Experimental source: strain FR137
R:Huang, I.Y.; Hughes, J.L.; Bergdoll, M.S.; Schantz, E.J.
J. Biol. Chem. 262, 7006-7013, 1987
A:Title: Complete amino acid sequence of staphylococcal enterotoxin A.
A:Reference number: A29566; MUID:87222293; PMID:3584106
A:Accession: A29566
A:Molecule type: protein
A:Residues: 25-241, 'S', 243-257 <HUA>
C:Genetics:
A:Gene: entA
A:Map position: 6
C:Superfamily: enterotoxin B

```
Query Match      20.8%; Score 251.5; DB 2; Length 257;  
Best Local Similarity 29.9%; Pred. NO. 3..5e-12;  
Matches 58; Conservative 40; Mismatches 59; Indels ~ 37; Gaps  
       7;
```

QY	44 YSDIVIDFKTSHNLVTKKLDVRDARDFINSEMDVEYAANDFTGDKTA VSVPPDNWLS 103
: : :	: : :
DB	-- --DSKDVIKYKGKVDLGY-- --YGQC 120
QY	104 KG---KVTATYYGGITPYQKTSI--PKNIPVNWLINGKSISVPYNFNEISTNKTTVTAQEID 158
: : :	: : : :
DB	121 AGGTPNKTACMYGGTVLHDNNRLTEERKKVIPINLWDLGKQTNPLETVKTNKNNTVGELD 180
QY	159 LKYRKLFIAGHQLYSS---GSYSYSGSLRVLPHTNDNSDKYSFDLFYPVGRKESIFKVVKD 215
: : :	: : :
DB	181 LOARRYLOEKXNYLNVDVFPGKVQRGLVLPHPTS-TSPSVNYDLEFGAOGQSNTLLRIYRD 239
QY	216 NKFENIDKIGHLDI 229
: : :	:
DB	240 KNTINSNM-HIDI 252

```

RESULT 7
A33953
enterotoxin D precursor - Staphylococcus aureus
C;Species: Staphylococcus aureus
C;Date: 09-Mar-1990 #sequence_revision 09-Mar-1990 #text_change 15-Oct-1999
C;Accession: A33953
J. Bacteriol. 171, 4799-4806, 1989
A;Title: Genetic and molecular analyses of the gene encoding staphylococcal enterot
A;Reference number: A33953; MUID:89359112; PMID:2549000
A;Accession: A33953
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-258 <BAV>
A;Cross-references: GB:M28521; NID:g1492109; PIDN:AB06195.1; PID:g758691
C;Superfamily: enterotoxin B

Query Match      20.8%; Score 251; DB 2; Length 258;
Best Local Similarity 29.4%; Pred. No. 3 8e-12;
Matches 77; Conservative 57; Mismatches 86; Indels 42; Gaps 13;

QY 1 MKKTKLIFS---FTSIFIAIISRPFVGLEVDNN-----SLLRNIYSTIVVEY 44
||| :: ||| : | : : : : : : : : : : : : : : : : : : : : : : :
Db 1 MKKFENILALLFTTSIVISPLN----VRANENIDSVKELHKHKKSELSSTALNNKHYS 55

```

QY	45	SD	---	IVDFKTS	-----	HNLVTKKL	-	DVRDAROFFINSENDEYAAANDFTKDGRIAYF	93
Db	56	ADRNPIIGENKSGDGFLENTLYKFFFTDLINFEDLLNFNSKENAQH-FKS-KWVDVY	113						
QY	94	SVFDDNN-YLSKQKVTAITYVGTTPQ--KTSIPKNIPVNLWINGKQISVPYNEISTNKT	150						
Db	114	PIRYSINCYGGEIDRTACTYGGVTPHEGNKLKERKKIPINLWINGVQKEVSLDKYQTDKK	173						
QY	151	TVTAQAEIDLKVRFLIAQHOLYSS---GSSYKSGRLVFTWNNDSKYSFDLFYVGRDKE	207						
Db	174	NVTVQELDAQARYLQKDLKLYNNDTLGGKIQRGKIEFDSSDGS-KVSYDLEFDVKGDPE	232						
QY	208	SIFKTVYKDNKSFNIDKIGHLDI	229						
Db	233	KOLRIYSDNKNLTSTEHL-HIDI	253						

RESULT 8
 C89984
 enterotoxin p [imported] - *Staphylococcus aureus* (strain N315),
 C:Species: *Staphylococcus aureus*
 C:Date: 10-May-2001
 C:Update: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001
 C:Accession: C89984
 R:Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, H.; Mizutani-U, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Seki-
 ma, A.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
 Lancet 357, 1225-1240, 2001
 A:Title: Whole genome sequencing of methicillin^r-resistant *Staphylococcus aureus*.
 A:Reference number: A89758; MUID:21311952; PMID:11418146
 A:Accession: C89984
 A:Status: preliminary
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-260 <KUR>
 A:Cross-references: GB:BA000018; PID:g13701743; PIDN:BAB43036.1; GSPDB:GN001449
 A:Experimental source: strain N315
 C:Genetics:
 C:Gene: sep
 C:Superfamily: enterotoxin B

```

Query Match      19.1%; Score 231; DB 2; Length 260;
Best Local Similarity 28.1%; Pred. NO. 1.3e-10;
Matches 73; Conservative 48; Mismatches 97; Indels 42; Gaps 13;

QY 2 KKTKLIFGFTSFYAIISR-----VFGLEVDNNS-----LLRNIYTIIVEYSD 46
      | | | | | : | : | : | : | : | : | : | : | : | : | : | : |
DB 6 KTFIFLLSF--IAITLIISPEVNGSEKSEINGKDLQKSELQGTALSRLGT--YHNGS 62

```

QY 47 IVIDFKTSHNLVTKKLDVRDARDFINSEM-----DEYAANDFKTGKIAVFSVPF 97
Db 63 ALIENKESNDQFLKNTIL--FNDFGTGHQWYNDLLVDLGSKDTANIYK-GKKVDLYGVY 119
QY 98 DNNYLSKGV---TAYTGGITPYOKTSI--PKNTIPVNLWINGKQISVYPYNEISNKTIV 152
Db 120 --GYOCTGTPKTAACMTGGVTLHDNNQLEEKVPIINLWDGKONTVPLGFPVKTAKREV 177
QY 153 TAEIDKLVKRLIAHQHOLYSS--GSSVYSGRLVFHTNDNSDKYSFDLFFVGVYRKESI 209
Db 178 TVQELDLSRHLVHTYNYLNTDAFNGIKQIRGLIEFHPIS-SGDSVGYDLFGAQQGYPTQ 236
QY 210 FKVKDNKSFNTDKIGHLDI 229
Db 237 LRIYRDNKTIK-SKNHIDI 255

RESULT 9

S18789
exotoxin A precursor (allele 4) - Streptococcus pyogenes (strain MGAS262 isolate California)
N:Alternate names: scarlet fever toxin
C:Species: Streptococcus pyogenes
A:Variety: strain MGAS262 isolate California
C:Date: 29-Jan-1993 #sequence_revision 29-Jan-1993 #text_change 16-Jul-1999
C:Accession: S18789
J. Nelson, K.; Schlievert, P.M.; Selander, R.K.; Musser, J.M.
J. Exp. Med. 174, 1271-1274, 1991
A:Title: Characterization and clonal distribution of four alleles of the speA gene encoded by strain MGAS262 isolate California
A:Reference number: S18782; MUID:92044323; PMID:1940804
A:Accession: S18789
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-236 <NE>
A:Cross-references: EMBL:X61573; NID:947303; PIDN:CAA43771.1; PID:947304
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991
C:Genetics:
A:Gene: speA
C:Superfamily: enterotoxin B
C:Keywords: exotoxin
F:1-22/Domain: signal sequence (fragment) #status predicted <SIG>
F:23-236/Product: exotoxin A (fragment) #status predicted <MAT>

Query Match 17.4%; Score 210.5; DB 2; Length 236;
Best Local Similarity 29.4%; Pred. No. 4.5e-09;
Matches 73; Conservative 47; Mismatches 77; Indels 51; Gaps 13;

QY 5 KLIFSFTSHNLV-ISRPFVGLVDNNSL-----LRNIYSFIVVEYSDIV----- 48
Db 2 KIVFVLAIFLGLTTSQEVFAQQDPNPSQLHRSSLVKRLQNIY--FLYEGDPVWHENYKS 59
QY 49 IDFKTSHNLV-----TKLDVRDARDFINSEMDEYAANDFKTGKIAVFSVPF 97
Db 60 VDQLLSHLIYVNSGLNVDKLTTELKKNEMSTLFPKNVD-----IYGEY 105
QY 98 DNN-YLSK-GKVTAYTGGITPYO--KTSIPKNTIPVNLWINGKQISVYPYNEISNKTIVT 153
Db 106 YHCHYCLNNAKRRACIYGGVTNHGHNHLEIPKILVNVKSIDGIQ-SLSF-DIETSKKMT 163
QY 154 AQEIDLKVRKFLIAHQHOLYSSG-SYKSGRLVFHTNDNSDKYSFDLFFVGVYRKESIFKV 212
Db 164 AQEIDLKVRKFLHTDNKQITNGSPKRYETGYIKFISKD-KETFWDFDFPEPEFNQVLYMI 222
QY 213 YKDNKSFN 220
Db 223 YKDNETLD 230

RESULT 10

S18786
exotoxin type A precursor (allele 2) - Streptococcus pyogenes phage (strain MGAS250 isolate California)
N:Alternate names: scarlet fever toxin
C:Species: Streptococcus pyogenes phage
A:Variety: strain MGAS250 isolate California; strain MGAS251 isolate California; strain

isolate United Kingdom; strain MGAS496 isolate Germany
C:Date: 29-Jan-1993 #sequence_revision 29-Jan-1993 #text_change 16-Jul-1999
C:Accession: S18786; S18787; S18788; S18790; S18792; S18795; S18799
A:Nelson, K.; Schlievert, P.M.; Selander, R.K.; Musser, J.M.
J. Exp. Med. 174, 1271-1274, 1991
A:Title: Characterization and clonal distribution of four alleles of the speA gene encoded by strain MGAS250 isolate California
A:Reference number: S18782; MUID:92044323; PMID:1940804
A:Accession: S18786
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-236 <NE>
A:Cross-references: EMBL:X61561; NID:947297; PIDN:CAA43759.1; PID:947298
A:Experimental source: strain MGAS250 isolate California unassigned phage
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991
C:Genetics:
A:Gene: speA2
C:Superfamily: enterotoxin B
C:Keywords: exotoxin
F:1-22/Domain: signal sequence (fragment) #status predicted <SIG>
F:23-236/Product: exotoxin type A (fragment) #status predicted <MAT>
Query Match 16.5%; Score 199.5; DB 2; Length 236;
Best Local Similarity 30.7%; Pred. No. 3.1e-08;
Matches 74; Conservative 48; Mismatches 78; Indels 45; Gaps 16;
QY 5 KLIFSFTSHNLV-ISRPFVGLVDNNSLNRNIYST-IVVEYSDIV-----ID 50
Db 2 KIVFVLAIFLGLTTSQEVFAQQDPNPSQLHRSSLVKRLQNIYFLYEGDPVWHENYKSD 61
QY 51 FKTSNHLVTK-----KLDVRDARDFINSEMDEYAANDFKTGDK-IAVFSVP-FDW 99

QY 5 KLIFSFTSIFAI-ISRVPFG-----LEVNNSLRNIIYST-IIVYESDIV-----ID 50
 :||| : || : |::| : |::| : |::| :
Db 2 KWPFVLVTFLGLTISQEVAQQDPDPSQLHRSLSLVKNLQNIFYLEGDPVTHENKVSVD 61
 :||| : || : |::| : |::| : |::| :
QY 51 EKTSNHLVTK-----KL DYRDARDFINSEMDEYAANDFKTGDK-IAVESVP-FDW 99
 :||| : || : |::| : |::| : |::| :
Db 62 QLUSHDIYNVSGNYDKLTAKELK-----NOEM----ATLFK--DKNIDIYGVEYYHL 108
 :||| : || : |::| : |::| : |::| :
QY 100 NYL-SKGKVAYTYGGITPYQ--KTSIPKNIPNLWMINGNQISVPVNEISTNKTTVTAOE 156
 :||| : || : |::| : |::| : |::| :
Db 109 CYLCENAERSACIYGVTVNEGHNLEPKKI VVKVSDIGIQ-SLSF-DIETNKKMWTAE 166
 :||| : || : |::| : |::| : |::| :
QY 157 IDLKVRFLAQHOLYSG--SSYKSGLVPHHTWNSDKYSFDLYFYGYRDKSEIFKYKD 215
 :||| : || : |::| : |::| : |::| :
Db 167 LDYKVRKYLTDNKLQXTNGSPSKYTGYIKF-IPKNKESEWFDFPPEPTQSRYLMIIYKD 225
 :||| : || : |::| : |::| : |::| :
QY 216 NKSFN 220
 :||| : || : |::| : |::| : |::| :
Db 226 NETLD 230
 :||| : || : |::| : |::| : |::| :

RESULT 12

S29659
A:A: title: Streptococcus pyogenes phage T12
N: Alternate names: erythrotoxin; scarlet fever toxin
C: Species: Streptococcus pyogenes phage T12
C: Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C: Accession: S29659; S18782; S18784; S18785; S18791; S18796; S18797; S18800
R: Weeks, C.R.; Ferratti, J.J., 1986
Infect. Immun. 52, 144-150, 1986
A:A: title: Nucleotide sequence of the type A streptococcal exotoxin (erythrotoxin)
A:A: reference number: S29659; MUID: 86166804; PMID: 3514452
A:A: accession: S29659
A:Molecule type: DNA
A:Residues: 1-251 <WEB>
A:Cross-references: GB:040453; EMBL:M19350; NID:g1877426; PIDN:AAC48868.1;
R:Nelson, K.; Schlievert, P.M.; Selander, R.K.; Musser, J.M.
J. Exp. Med. 174, 1271-1274, 1991
A:A: title: Characterization and clonal distribution of four alleles of the strain
A:A: reference number: S18782; MUID: 92044323; PMID: 1940804
A:A: accession: S18782
A>Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 9-244 <NEL>
A:Cross-references: EMBL:X61560; NID:g47287; PIDN:CAA43758.1; PID:g47288
A:A: experimental source: Streptococcus pyogenes strain MGAS155 isolate Nebraska
A:A: note: The nucleotide sequence was submitted to the EMBL Data Library, Sep
A:A: accession: S18784
A>Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 9-244 <NEA>
A:Cross-references: EMBL:X61556; NID:g47291; PIDN:CAA43754.1; PID:g47292
A:A: experimental source: Streptococcus pyogenes strain MGAS165 isolate Minnesota
A:A: note: The nucleotide sequence was submitted to the EMBL Data Library, Sep
A:A: accession: S18785
A>Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 9-244 <NEZ>
A:Cross-references: EMBL:X61559; NID:g47293; PIDN:CAA43757.1; PID:g47294
A:A: experimental source: Streptococcus pyogenes strain MGAS167 isolate Texas
A:A: note: The nucleotide sequence was submitted to the EMBL Data Library, Sep
A:A: accession: S18791
A>Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 9-244 <NEY>
A:Cross-references: EMBL:X61555; NID:g47309; PIDN:CAA43753.1; PID:g47310
A:A: experimental source: Streptococcus pyogenes strain MGAS327 isolate Arizona
A:A: note: The nucleotide sequence was submitted to the EMBL Data Library, Sep
A:A: accession: S18796
A>Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 9-244 <NEO>
A:Cross-references: EMBL:X61557; NID:g47319; PIDN:CAA43755.1; PID:g47320

A;Accession: S18796
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 9-244 <NEO>
A;Cross-references: EMBL:X61557; NID:g47319; PIDN:CAA43755.1; PID:g47320

```

QY 29 NNSLLRIYGTI-----VYEYSDIVDFKTSNLTKKLDVRDARDFINSEMDEYAAAN 82
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 53 NDDYINNRFYTVKSIYSTTEKFLDFDLFISINWLDGISAEPKDLKVEFSSAI-----SK 108

QY 83 DFKTGDKIAVSPFDDNNYLSGKV-TAYTYGGITPYQ--KTSIPKNIPVNLWINGKQIS 139
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 109 EF-LGKTVDTYGVYKARHGEHQVDCTACTYGGVTPHNNKLSPEKNIGVAVYKD--NVN 165

QY 140 VPYNEISTNKTITTAQELDKVKFLAQHOLYS-SSGSYKSGRLVPH--NDNSDKYSFD 197
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 166 VNTFIVTDRKKVTAQELDKVTKLNNAKLYDRMTSDVQGYIKFHSHEKSEFYD 225

QY 198 LFVVGVDKESIFKVKDKNSFNIDKIGHLDI 229
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 226 LFYIKGNLPDQYLOIYNNDKTIDSSDY-HIDV 256

RESULT 14
H89968
enterotoxin Sen [imported] - Staphylococcus aureus (strain N315)
C:Species: Staphylococcus aureus
C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001
C:Accession: H89968
R:Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui,
ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimura,
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A:Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.
A:Reference number: A89758; MUID:21311952; PMID:11418146
A:Accession: H89968
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-258 <KUR>
A:Cross-references: GB:BA000018; PID:g13701618; PIDN:BAB42911.1; GSPDB:GN00149
A:Experimental source: strain N315
C:Genetics:
A:Gene: sen
C:Superfamily: enterotoxin B

Query Match 13.7%; Score 165.5; DB 2; Length 258;
Best Local Similarity 25.6%; Pred. No. 1.4e-05;
Matches 66; Conservative 53; Mismatches 102; Indels 37; Gaps 13;

QY 1 MKKTKLIFGTSIFI---AIISRPVFGLEVDDNSL-----LRNIYSTIVY-- 42
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 4 IKKLRLFYIAIIITLLCLINNNYNAEVDKDLAKKSLDSSKLFNTSYTDTIWQL 63

QY 43 -EYSDIVDFKTSNLTKKLDVRDARDFINSEMDEY-AANDFTGDKIAVSPFDWN 100
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 64 DESNKISTDQLLNTIILKNIDISVLKTSLSKVEFNSSDLANQFK-GKNIDIYGLYFGNK 122

QY 101 Y--LSGKGVTAYTYGGITPYQKTSI--PKNIPVNLWINGKQISVPYNE---TSTNKTITVT 153
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 123 CVGLTEEK-TSLYGGVTIHDGNQLDDEERKIVGNVNFQGVQ-----QEGFVTKTKAKVT 176

QY 154 AQBIDLKVKFLAQHOLYS--SVKSGRLVPH--NDNSDK-YSPDLFVVGVDKESIFK 211
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 177 VQELDKVKFKLENLYTKTKDGNIGKICIFHSHNHQDQSFYIDLYNVKSGVGAFFQ 236

QY 212 VYKDKNSFNIDKIGHLDI 229
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 237 FYSDNETVSSNY-HIDV 253

RESULT 15
ENSAB6
enterotoxin B precursor - Staphylococcus aureus
C:Species: Staphylococcus aureus
C:Date: 24-Apr-1984 #sequence_revision 15-Oct-1996 #text_change 18-Jun-1999
C:Accession: S27360; A92265; S27240; A01815
R:Jones, C.L.; Khan, S.A.
J. Bacteriol. 166, 29-33, 1986

```

A:Title: Nucleotide sequence of the enterotoxin B gene from *Staphylococcus aureus*.
 A:Reference number: S27360; MUID:8618029; PMID:3957869
 A:Accession: S27360
 A:Molecule type: DNA
 A:Residues: 1-266 <JON>
 A:Cross-references: EMBL:M11118; NID:g152999; PIDN:AAA88550.1; PID:g153000
 A:Experimental source: strain S6
 R:Huang, I.Y.; Bergdoll, M.S.
 J. Biol. Chem. 245, 3518-3525, 1970
 A:Title: The primary structure of staphylococcal enterotoxin B. III. The cyanogen bromide
 A:Reference number: A92065; MUID:71007902; PMID:5470821
 A:Accession: A92065
 A:Molecule type: protein
 A:Residues: 28-55, 'NND', 59-68, 'NE', 71, 'FDLYL', 78-117, 119-127, 'N', 129, 'D', 131-132, 'ENT',
 A:Experimental source: strain S-6
 R:Huang, I.Y.; Bergdoll, M.S.
 J. Biol. Chem. 245, 3511-3517, 1970
 A:Title: The primary structure of staphylococcal enterotoxin B. II. Isolation, composition
 A:Reference number: A92064; MUID:71007901; PMID:5470820
 A:Accession: A92064
 A:Molecule type: chymotryptic peptides
 R:Huang, I.Y.; Bergdoll, M.S.
 J. Biol. Chem. 245, 3493-3510, 1970
 A:Title: The primary structure of staphylococcal enterotoxin B. I. Isolation, composition
 A:Reference number: A92063; MUID:71007900; PMID:5470819
 A:Accession: A92063
 A:Molecule type: tryptic peptides
 R:Schantz, E.J.; Roessler, W.G.; Wagman, J.; Spero, L.; Dunnehy, D.A.; Bergdoll, M.S.
 Biochemistry 4, 1011-1016, 1965
 A:Title: Purification of staphylococcal enterotoxin B.
 A:Reference number: A90548; MUID:66035792; PMID:4953912
 A:Accession: A90548
 A:Molecule type: biological source of protein
 R:Alakhov, V.Y.; Klinsky, E.Y.; Kolosov, M.I.; Maurer-Fogy, I.; Moskaleva, E.Y.; Sveshnik
 Eur. J. Biochem. 209, 823-828, 1992
 A:Title: Identification of functionally active fragments of staphylococcal enterotoxin B
 A:Reference number: S27240; MUID:93049338; PMID:1425690
 A:Accession: S27240
 A:Molecule type: protein
 A:Residues: 28-42; 128-148 <ALA>
 C:Superfamily: enterotoxin B
 C:Keywords: enterotoxin; extracellular protein; toxin
 F:1-27/Domain: signal sequence #status predicted <SIG>
 F:28-266/Product: enterotoxin B #status experimental <MAT>
 F:120-140/Disulfide bonds: #status experimental

Query Match 13.5%; Score 162.5; DB 1; Length 266;
 Best Local Similarity 25.4%; Pred. No. 2.6e-05;
 Matches 57; Conservative 40; Mismatches 86; Indels 41; Gaps 9;

QY 28 DNNSLLRNIYSTIVYEYSIVIVDFKT-----SHNLYTKKLDVRDARDFINSEHDEYAAND 83
 Db 57 DNHVSAINVKSIDQFLYFDLIYSIKDTKLGNDVNRVFEKKNLADKYDKYDVFEGANY 116
 QY 84 F-----RTGDKIAVFSVPFDMNLSKGVATYTYGGITPYOKTSIPK--NIPVNLWIN 134
 Db 117 YVOCYFSKKTN-----DINSHQTDKRTKCTMGVTEHNGNQLDKYRSITVRVFE 166
 QY 135 GQKISVPYNEISTNKTVTTAQEIIDLKVRKFLIAQHOLYS-SGSSYKSGRLVFHTNDNSDK 193
 Db 167 GKNLL--SFDVQTNKKKTAQELDYLRHVLVKNKKLYEFNNSPYETGYIKFTENENSF 224
 QY 194 YSF-----DLFVYGVYEDKESIFKVKDKNSFNIDKIGHLDIEID 232
 Db 225 YDMMPAPGDKF-----DQSKYLMYNDNK-----MVDSDKDVRIE 258

Search completed: February 14, 2003, 13:46:12
 Job time : 21 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: February 14, 2003, 13:44:04 ; Search time 12 seconds

(without alignments)

805.332 Million cell updates/sec

Title: US-09-869-136-2

Perfect score: 1207

Sequence: 1 MKYTKLIFSTSFIAISR.....KDNKSFNIDKIGHLDIEIDS 233

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	305	25.3	235	1	SPEC_STRPY
2	258.5	21.4	257	1	ETXE_STAAU
3	251.5	20.8	257	1	ETXA_STAAW
4	251	20.8	258	1	ETXD_STAAU
5	243	20.1	234	1	SPEC_STRPY
6	203	16.8	236	1	SPEH_STRPY
7	195.5	16.2	251	1	SPEA_STRPY
8	162.5	13.5	266	1	ETXB_STAAU
9	161	13.3	258	1	ETXC_STAAU
10	158	13.1	266	1	ETC2_STAAU
11	156	12.9	266	1	ETC3_STAAU
12	153.5	12.7	266	1	ETC1_STAAU
13	112.5	9.3	234	1	TSST_STAAU
14	106.5	8.8	1010	1	YK11_CAEEL
15	103	8.5	1216	1	YK15_CAEEL
16	100.5	8.3	532	1	60IN_BUCAI
17	93.5	7.7	444	1	TIG_MYCPN
18	93	7.7	691	1	LCN3_LACLA
19	93	7.7	823	1	AXL2_YEAST
20	91.5	7.6	645	1	REP_BUCAI
21	91	7.5	380	1	RMAR_WILMR
22	91	7.5	386	1	VC17_VACCC
23	91	7.5	760	1	ETF2_MSEPV
24	88	7.3	667	1	Y366_MYCGE
25	87.5	7.2	602	1	EXSA_BUCAI
26	87.5	7.2	1155	1	IFP2_METJA
27	87.5	7.2	1276	1	BXD_CLOBO
28	87	7.2	540	1	MTA1_ACICA
29	86.5	7.2	590	1	MSP_TRELE
30	86.5	7.2	905	1	YD83_HUMAN
31	86	7.1	415	1	CC11_YEAST
32	86	7.1	1616	1	SLAP_BACCI
33	86	7.1	3744	1	YHP9_YEAST

ALIGNMENTS

RESULT 1

ID	SPEC_STRPY	STANDARD;	PRT;	235 AA.
DT	P13380;			
DT	01-JAN-1990 (Rel. 13, Created)			
DT	16-OCT-2001 (Rel. 40, Last sequence update)			
DT	16-OCT-2001 (Rel. 40, Last annotation update)			
DE	Exotoxin type C precursor (SPE C).			
GN	SPEC OR SPY0711.			
OS	Streptococcus pyogenes.			
OC	Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;			
OC	Streptococcus.			
OX	NCBI_TaxID=1314;			
RN	[1]			
RP	SEQUENCE FROM N.A., AND SEQUENCE OF 28-52.			
RC	SERAIN-1488 / NCBI=1383			
RX	MEDLINE=88314303; Pubmed=3045005;			
RA	Goshorn S.C., Schlievert P.M.;			
RT	"Nucleotide sequence of streptococcal pyrogenic exotoxin type C."			
RL	Infect. Immun. 56:2518-2520(1988).			
RN	[2]			
RP	REVISIONS TO 21-26			
RC	STRAIN-T18P / MGAS 1581			
RX	MEDLINE=92363541; Pubmed=1568157;			
RA	Kapur V., Nelson K., Schlievert P.M., Selander R.K., Musser J.M.;			
RT	"Molecular population genetic evidence of horizontal spread of two alleles of the pyrogenic exotoxin C gene (speC) among pathogenic clones of Streptococcus pyogenes."			
RL	Infect. Immun. 60:3513-3517(1992).			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN-SF370 / ATCC 700294 / Serotype M1;			
RX	MEDLINE=21192684; Pubmed=11296296;			
RA	Ferretti J.J., McShan W.M., Aldic D.J., Savic D.J., Savic G., Lyon K.,			
RT	Primeaux C., Gerate S., Savorov A.N., Kenton S., Lal H.S., Lin S.P.,			
RL	Qian X., Jia H.G., Najjar F.Z., Red O., Zhu H., Song L., White J.,			
RY	Yuan X., Clifton S.W., Roe B.A., McLaughlin R.;			
RT	"Complete genome sequence of an M1 strain of Streptococcus pyogenes."			
RL	Proc. Natl. Acad. Sci. U.S.A. 98:4658-4663(2001).			
RN	[4]			
RP	X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS) OF 30-215			
RX	MEDLINE=97397332; Pubmed=9253413;			
RA	Roussel A., Anderson A.F., Baker H.M., Fraser J.D., Baker E.N.;			
RT	"Crystal structure of the streptococcal superantigen SPE-C:			
RT	dimerization and zinc binding suggest a novel mode of interaction with MHC class II molecules."			
RL	Nat. Struct. Biol. 4:635-643(1997).			
CC	- - SUBUNIT: Binds to major histocompatibility complex class II beta chain.			
CC	- - DISEASE: THE STREPTOCOCCAL PYROGENIC TOXINS A, B, AND C ARE THE CAUSATIVE AGENTS OF THE SYMPTOMS ASSOCIATED WITH SCARLET FEVER, HAVE BEEN ASSOCIATED WITH STREPTOCOCCAL TOXIC SHOCK-LIKE DISEASE AND MAY PLAY A ROLE IN THE EARLY EVENTS OF RHEUMATIC FEVER.			
CC	- - MISCELLANEOUS: THIS TOXIN SEEMS TO BE CODED BY A BACTERIOPHAGE.			

34	85.5	7.1	530	1	TP6B_SULSO
35	85.5	7.1	997	1	P257_ECOLI
36	85	7.0	303	1	Y114_MERJA
37	85	7.0	617	1	Y237_BUCAI
38	85	7.0	1085	1	IFH1_YEAST
39	84.5	7.0	335	1	Y063_BORBU
40	84.5	7.0	413	1	YP71_MYCMY
41	84.5	7.0	428	1	G6P1_MYGGA
42	84.5	7.0	841	1	PSPI_YEAST
43	84	7.0	970	1	Y087_BUCAI
44	84	7.0	1157	1	C8AA_BACUK
45	83.5	6.9	1901	1	YCF1_TOBAC

Q97zf0	sulfolobus
P25239	escherichia
Q57578	methanococc
P57331	buchnera ap
P39520	saccharomyc
O51090	borrelia bu
P5802	mycoplasma
Q6x58	mycoplasma
P50896	saccharomyc
P37189	buchnera ap
Q45704	bacillus th
P12222	nicotiana t


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J. Bacteriol. 170:2954-2960(1988).
[2]
3D-STRUCTURE MODELING.
MEDLINE-96022987; PubMed-7552730;
Svaminathan S., Furey W.F. Jr., Pletcher J., Sax M.;
"Residues defining V beta specificity in staphylococcal
enterotoxins.";
Nat. Struct. Biol. 2:680-686(1995).
CC CC COFACTOR: Binds 1 zinc ion per subunit. The zinc ion is necessary
for the toxin interaction with MHC class II (By similarity).
CC CC -1- SUBCELLULAR LOCATION: Secreted.
CC CC -1- DISEASE: STAPHYLOCOCCAL ENTEROTOXINS CAUSE THE INTOXICATION
STAPHYLOCOCCAL FOOD POISONING SYNDROME.
CC CC -1- SIMILARITY: BELONGS TO THE STAPHYLOCOCCAL/STREPTOCOCCAL TOXIN
FAMILY.
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EMBL; M21319; AAA26617.1; -.
DR DR PIR; A28179; A28179.
DR DR PDB; 1SEE; 15-OCT-95.
DR DR InterPro; IPR001961; Staph/Strep_toxin.
DR DR Pfam; PF01123; Staph_Strp_toxin; 1.
DR DR Pfam; PF02876; Staph_Strp_tox_C; 1.
DR DR PRINTS; PR00279; BACTRLTOXIN.
DR DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
DR DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
KW Enterotoxin; Toxin; Signal; Superantigen; Metal-binding; Zinc;
KW 3D-structure. 1 27
FT SIGNAL 1 27 ENTEROTOXIN TYPE E.
FT CHAIN 28 257
FT METAL 211 211 ZINC (BY SIMILARITY).
FT METAL 249 249 ZINC (BY SIMILARITY).
FT METAL 251 251 ZINC (BY SIMILARITY).
FT SEQUENCE 257 AA; 29358 MW; 27EDA94897770CE3 CRC64;
Query Match 21.4%; Score 258.5; DB 1; Length 257;
Best Local Similarity 26.4%; Pred. No. 1.3e-13;
Matches 75; Conservative 55; Mismatches 67; Indels 87; Gaps 13;
QY 1 MKYTKLIFSTSFIA--IISRPVG-----LEVNNSL--LRNIY--- 37
||||| : : : : : : : : : : : : : : : : : :
DB 1 MKKTAPIL---LLFIALTLTSPLVNGSEKSEINEKDLKKKSELORNLSLRQIYYN 57
QY 38 -----STIVYE-----YSDIVIDFKTSHNLVTKKLDVDRDARDFIN 73
||||| : : : : : : : : : : : : : : : : : :
DB 58 EKAITENKSDDOFLENTLLKFGFTGHWPNDLVYD-----LGSKDATNKYKG 106
QY 74 SEMDEYAANDFKTGDKIAVFSVPFDNNYLSKG---KVTAYTYGGITPYQKTSI--PKNIP 128
: : : : : : : : : : : : : : : : : : : : : : : :
DB 107 KKVDLYGAY-----YGYQCAGGTPNKTCMAGVGLHDNNRLTEKKVP 150
QY 129 VNLWINGKQISVPYNEISNTKTTVTAQETDLKVKRLIAHQHLYSS---GSSYKSGRLVF 185
||||| : : : : : : : : : : : : : : : : : : : : : : : :
DB 151 INLWDGKQTTVPIDKVKTSKKEVTQVEDLQARHVLHGKFLGSLDSFGGKVGQRLIVE 210
QY 186 HTNNDNSDKYSFDLFYGVYGRDKESIFKVKYKDNKSNFDKIGHLDI 229
: : : : : : : : : : : : : : : : : : : : : : : :
DB 211 HSSEGS-TVSYVLDFAQQGVPDPLLRIYRDNKTINSNL-HIDL 252
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RESULT 3
ID ETXA_STAAW STANDARD; PRT; 257 AA.
AC P13163;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)

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15-JUN-2002 (Rel. 41, Last annotation update)
DE Enterotoxin type A precursor (SEA).
GN ENTA OR MW1889.
OS Staphylococcus aureus (strain MW2), and
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=196620, 1280;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MM2;
RX MEDLINE=12040717; PubMed=12044378;
RA Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A.,
RA Negai Y., Iwama N., Asano K., Naimi T., Kuroda H., Cui L.,
RA Yamamoto K., Hiramatsu K.;
RA "Genome and virulence determinants of high virulence community-
RT acquired MRSA";
RL Lancet 359:1819-1827(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=MM2;
RX MEDLINE=88086892; PubMed=3335483;
RA Betley M.J., Mekalanos J.J.;
RA "Nucleotide sequence of the type A staphylococcal enterotoxin gene";
RL J. Bacteriol. 170:34-41(1988).
RN [3]
RP SEQUENCE OF 25-257.
RX MEDLINE=87222293; PubMed=3584106;
RA Huang I.-Y., Hughes J.L., Bergdoll M.S., Schantz E.J.;
RA "Complete amino acid sequence of staphylococcal enterotoxin A.";
RL J. Biol. Chem. 262:7006-7013(1987).
RN [4]
RP X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).
RX MEDLINE=95354648; PubMed=7628431;
RA Schad E.M., Zaitseva I., Zaitsev V.N., Dohlsten M., Kalland T.,
RA Schlievert P.M., Ohlendorf D.H., Svensson L.A.;
RA "Crystal structure of the superantigen staphylococcal enterotoxin
RL type A.";
RL EMBO J. 14:3292-3301(1995).
RN [5]
RP X-RAY CRYSTALLOGRAPHY (2.7 ANGSTROMS).
RX MEDLINE=97113025; PubMed=8943278;
RA Sundstroem M., Hallen D., Svensson A., Schad E., Dohlsten M.,
RA Abrahamson L.;
RA "The Co-crystal structure of staphylococcal enterotoxin type A with
RT Zn2+ at 2.7-A resolution. Implications for major histocompatibility
RT complex class II binding.";
RL J. Biol. Chem. 271:32212-32216(1996).
RN [6]
RP 3D-STRUCTURE MODELING.
RX MEDLINE=96022987; PubMed=7552730;
RA Swaminathan S., Furey W.F. Jr., Pletcher J., Sax M.;
RA "Residues defining V beta specificity in staphylococcal
RT enterotoxins.";
RL Nat. Struct. Biol. 2:680-686(1995).
RN [7]
RP COMPARISON OF STRUCTURE OF SEA AND SEC2.
RX MEDLINE=97334373; PubMed=9191070;
RA Schad E.M., Papageorgiou A.C., Svensson L.A., Acharya K.R.;
RA "A structural and functional comparison of staphylococcal
RT enterotoxins A and C2 reveals remarkable similarity and
RT dissimilarity.";
RL J. Mol. Biol. 269:270-280(1997).
CC -1- COFACTOR: Binds 1 zinc ion per subunit. The zinc ion is necessary
CC for the toxin interaction with MHC class II.
CC -1- SUBUNIT: MONOMER.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- DISEASE: STAPHYLOCOCCAL ENTEROTOXINS CAUSE THE INTOXICATION
CC STAPHYLOCOCCAL FOOD POISONING SYNDROME.
CC -1- MISCELLANEOUS: THIS TOXIN SEEMS TO BE CODED BY A BACTERIOPHAGE.
CC -1- SIMILARITY: BELONGS TO THE STAPHYLOCOCCAL/STREPTOCOCCAL TOXIN
CC FAMILY.
CC -----
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SPEL_STRPY STANDARD; PRT; 236 AA.

AC Q9X5C8;

DT 16-OCT-2001 (Rel. 40, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 15-JUN-2002 (Rel. 41, Last annotation update)

DE Exotoxin type H precursor (SPE H).

GN SPEH OR SPY1008

OS Streptococcus pyogenes.

OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;

OC Streptococcus.

OX NCBI_TaxID=1314;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=M15;

RX MEDLINE=99093428; PubMed=9874566;

RA Proft T., Moffatt S.L., Berkahn C.J., Fraser J.D.;

RT "Identification and characterization of novel superantigens from

RT Streptococcus pyogenes."

RL J. Exp. Med. 189:89-102(1999).

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN=SF370 / ATCC 700294 / Serotype M1;

RX MEDLINE=21192684; PubMed=11296296;

RA Ferretti J.J., McShan W.M., Ajdic D.J., Savic D.J., Savić G., Lyon K.,

RA Primeaux C., Sezate S., Suvorov A.N., Kenton S., Lal H.S., Lin S.P.,

RA Qian Y., Jia H.G., Najjar F.Z., Ren Q., Zhu H., Song L., White J.,

RA Iuan X., Clifton S.W., Roe B.A., McLaughlin R.;

RT "Complete genome sequence of an M1 strain of Streptococcus pyogenes."

RL Proc. Natl. Acad. Sci. U.S.A. 98:4658-4663(2001).

CC -1- SUBUNIT: Bands to major histocompatibility complex class II beta

CC chain.

CC -1- SUBCELLULAR LOCATION: Secreted.

CC -1- DISEASE: Mitogenic for human peripheral blood lymphocytes.

CC -1- SIMILARITY: BELONGS TO THE STAPHYLOCOCCAL/STREPTOCOCCAL TOXIN

CC FAMILY.

CC -----

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DR EMBL; AF124500; AAD30989.1; -

DR EMBL; AE006546; AAK33907.1; -

DR HSP; P13163; 1SXT.

DR InterPro: IPR001961; Staph/Strep_toxin.

DR Pfam; PF01123; Staph_Strep_toxin; 1.

DR Pfam; PF02876; Staph_Strep_toxin; 1.

DR PROSITE; P500277; STAPH_STREP_TOXIN_1; FALSE_NEG.

DR PROSITE; P500278; STAPH_STREP_TOXIN_2; 1.

KW Toxin; Signal; Complete proteome.

FT SIGNAL 1 32

FT CHAIN 33 236

FT SEQUENCE 236 AA; 27485 MW; 16352923907AD40D CRC64;

Query Match. 16.8%; Score 203; DB 1; Length 236;

Best Local Similarity 27.5%; Pred No. 2.9e-09;

Matches 65; Conservative 43; Mismatches 78; Indels 50; Gaps 12;

QY 34 RNIYSTIV---YEYSDIV---IDFKTSHNL-----VTKLDVDRDARDFINSEM 76

DB 12 KKIYSMIICLSFLYSNVVQANSYNTNRHNLSELYKHDSNLLEADSIKNSPD-IYVSHM 70

QY 77 DEYAANDFTGDKIAVSPVDFDNYLSK-----GKVYAY-----TYGGIT 116

DB 71 LKYSVKD-----KNLSVF-----FEKDIQSQEFKDEVDIYALSAQECVCEPKRYEAFGGIT 123

QY 117 PYOKTSIPKNIPVNIWNGKQISVPYNEISTNKTNTTAQIEDLKVKRFLAQHQLYSS-G 175

DB 124 LTNSEKKEIKVPVNWMDKSKQ---OPPMFIVNKPVTQAQEVVDIKVRKLLIKKYDIYNRE 181

QY 176 SSYSKGRLVFHTNDNSKYSFDFYGVGYDRKESIFKVKYKDKNSFKHLDIEI 231

DB 182 QKYSKGTVTLDNSGKD-IVFDLYVFGNGDFNSMLKIYSNNRIDSTQF-HVDYSI 235

RESULT 7

SPEL_STRPY ID SPEL_STRPY STANDARD; PRT; 251 AA.

AC P08095;

DT 01-AUG-1988 (Rel. 08, Created)

DT 01-JAN-1990 (Rel. 13, Last sequence update)

DT 15-JUN-2002 (Rel. 41, Last annotation update)

DE Exotoxin type A precursor (Scarlet fever toxin) (Erythrogenic toxin)

DE (SPE A).

GN SPEA OR SPY18_0393.

OS Streptococcus pyogenes, and

OS Streptococcus pyogenes (serotype M18).

OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;

OC Streptococcus.

OX NCBI_TaxID=1314, 186103;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=86166804; PubMed=3514452;

RA Weeks C.R., Ferretti J.J.;

RT "Nucleotide sequence of the type A streptococcal exotoxin

RT (erythrogenic toxin) gene from Streptococcus pyogenes bacteriophage

RT T12."

RL Infect. Immun. 52:144-150(1986).

RN [2]

RP SEQUENCE FROM N.A.

RX MEDLINE=86284313; PubMed=3526093;

RA Johnson L.P., L'Italien J.J., Schlievert P.M.;

RT "Streptococcal pyrogenic exotoxin type A (scarlet fever toxin) is

RT related to staphylococcus aureus enterotoxin B."

RL Mol. Gen. Genet. 203:354-356(1986).

RN [3]

RP SEQUENCE FROM N.A.

RC STRAIN=MGAS8232 / Serotype M18;

RX MEDLINE=21927593; PubMed=11917108;

RA Smoot J.C., Barbican K.D., Van Gompel J.J., Smoot L.M., Chaussee M.S.,

RA Sylva G.L., Sturdevant D.E., Ricklefs S.M., Porcella S.F.,

RA Parvins L.D., Beres S.B., Campbell D.S., Smith T.M., Zhang Q.,

RA Kapur V., Daly J.A., Veasy L.G., Musser J.M.;

RT "Genome sequence and comparative microarray analysis of serotype M18

RT group A Streptococcus strains associated with acute rheumatic fever

RT outbreaks."

RL Proc. Natl. Acad. Sci. U.S.A. 99:4668-4673(2002).

RN [4]

RP X-RAY CRYSTALLOGRAPHY (2.57 ANGSTROMS).

RX MEDLINE=99094887; PubMed=9878045;

RA Papageorgiou A.C., Collins C.M., Gutman D.M., Kline J.B.,

RA O'Brien S.M., Tranter H.S., Acharya K.R.;

RT "Structural basis for the recognition of superantigen streptococcal

RT pyrogenic exotoxin A (SpeA) by MHC class II molecules and T-cell

RT receptors."

RL EMBO J. 18:9-21(1999).

CC -1- SUBUNIT: Binds to major histocompatibility complex class II beta

CC chain.

CC -1- DISEASE: THE STREPTOCOCCAL PYROGENIC TOXINS A, B, AND C ARE

CC THE CAUSATIVE AGENTS OF THE SYMPTOMS ASSOCIATED WITH SCARLET

CC FEVER, HAVE BEEN ASSOCIATED WITH STREPTOCOCCAL TOXIC SHOCK-LIKE

CC DISEASE AND MAY PLAY A ROLE IN THE EARLY EVENTS OF RHEUMATIC

CC FEVER.

CC -1- MISCELLANEOUS: THIS TOXIN SEEMS TO BE CODED BY BACTERIOPHAGE T12.

CC -1- SIMILARITY: BELONGS TO THE STAPHYLOCOCCAL/STREPTOCOCCAL TOXIN

CC FAMILY.

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CC EMBL: U40453; AAC48868.1;
CC DR EMBL: X03929; CA27568.1;
CC DR EMBL: AE009982; AAL97141.1;
CC DR PIR: A26152; A26152.
CC DR PIR: S29659; S29659.
CC DR PDB: 1B12; 24-NOV-99.
CC DR InterPro: IPR001961; Staph/Strep_toxin.
CC DR Pfam: PF01123; Staph_Strp_toxin; 1.
CC DR Pfam: PF02876; Staph_Strp_toxin; 1.
CC DR PRINTS: PR00279; BACTRTOXIN.
CC DR PROSITE: PS00277; STAPH_STRP_TOXIN_1; 1.
CC DR PROSITE: PS00278; STAPH_STRP_TOXIN_2; 1.
CC KW Toxin; Signal; 3D-structure.
CC FT SIGNAL 1 30
CC FT CHAIN 31 251
CC FT DISULFID 117 128
CC FT CONFLICT 6 6
CC FT CONFLICT 17 18
CC FT CONFLICT 25 35
CC FT CONFLICT 40 40
CC FT CONFLICT 43 43
CC FT CONFLICT 47 59
CC FT CONFLICT 129 129
CC FT CONFLICT 165 178
CC FT CONFLICT 251 AA; 29246 MW; 54001FE4CCCCBFC3 CRC64;
CC SQ SEQUENCE 251 AA; 29246 MW; 54001FE4CCCCBFC3 CRC64;

Query Match 16.2%; Score 195.5; DB 1; Length 251;
Best Local Similarity 23.8%; Pred. No. 1.2e-08;
Matches 73; Conservative 48; Mismatches 79; Indels 45; Gaps 16;

QY 5 KLIFSFTSIPFAL-ISRPFVFG-----LEVNNLLRNIYST-IVYVSDIV-----ID 50
Db 10 KNVFFVLTFLGLTISQEVFAQDPDPSPQLHRSLVNLQNIYFLYEGDPVTHENVKSDV 69
QY 51 FKTSHNLVTK-----KLDVRDARDFEINSEMDVAANDFTGDK-IAVFSVP-FDW 99
Db 70 QLLSHDLIYNVSGPNYDKLTKELK-----NQEM-----ATLFK--DKNVDIYGVYYHL 116
QY 100 NYL-SKGKVATYTGITPYO--KTSIPKIPVNLWINGKOISVPYNEISTNKITVTAQE 156
Db 117 CYLCENABRSACIYGGVTHNHNHLEIPKIKVWKSIDIGQ-LSLF-DIETNKKWVTAQE 174
QY 157 IDLKVRFELIAQHLYSSG-SSYKSGRLVFTNDSNKSYPDLFYGVGRKESIFKVKYKD 215
Db 175 LDYKVRKYLTDNKLQTYNGPSKYETGIKF-IPKNKESFWDFPEPEFTQSKYLMYKD 233
QY 216 NKSFN 220
Db 234 NETLD 238

RESULT 8
ETXB STAAU
ID ETXB STAAU STANDARD; PRT; 266 AA.
AC P01552;
DT 21-JUL-1986 (Rel. 01, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Enterotoxin type B precursor (SEB).
GN ENTB.
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=8618029; PubMed=3957869;
RA Jones C.L., Khan S.A.;
RT "Nucleotide sequence of the enterotoxin B gene from Staphylococcus

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RT aureus.";
RL J. Bacteriol. 166:29-33(1986).
RN [2]
RP SEQUENCE OF 40-91 FROM N.A.
RX MEDLINE=85298255; PubMed=3898073;
RA Ranelli D.M., Jones C.L., Johns M.B., Mussey G.J., Khan S.A.;
RT "Molecular cloning of staphylococcal enterotoxin B gene in
RT Escherichia coli and Staphylococcus aureus.";
RL Proc. Natl. Acad. Sci. U.S.A. 82:5850-5854(1985).
RN [3]
RP SEQUENCE OF 28-266 (S-6).
RX MEDLINE=71007902; PubMed=5470821;
RA Huang I.-Y., Bergdoll M.S.;
RT "The primary structure of staphylococcal enterotoxin B. 3. The
RT cyanogen bromide peptides of reduced and aminoethylated enterotoxin
RT B, and the complete amino acid sequence.";
RL J. Biol. Chem. 245:3518-3525(1970).
RN [4]
RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS).
RX MEDLINE=93063291; PubMed=1436058;
RA Swaminathan S., Furey W.F. Jr., Fletcher J., Sax M.;
RT "Crystal structure of staphylococcal enterotoxin B, a superantigen.";
RL Nature 359:801-806(1992).
RN [5]
RP X-RAY CRYSTALLOGRAPHY (2.7 ANGSTROMS) OF COMPLEX WITH MHC II.
RX MEDLINE=94203282; PubMed=8152483;
RA Janderzky T.S., Brown J.H., Gorga J.C., Stern L.J., Urban R.G.,
RA Chi Y.I., Stauffer C., Strominger J.L., Wiley D.C.;
RT "Three-dimensional structure of a human class II histocompatibility
RT molecule complexed with superantigen.";
RL Nature 368:711-718(1994).
RN [6]
RP X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS) OF COMPLEX WITH TCR.
RX MEDLINE=95096298; PubMed=9881971;
RA Li H., Llera A., Tsuchiya D., Leder L., Ysern X., Schlievert P.M.,
RA Karjalainen K., Mariuzza R.A.;
RT "Three-dimensional structure of the complex between a T cell receptor
RT beta chain and the superantigen staphylococcal enterotoxin B.";
RL Immunity 9:807-816(1998).
RN [7]
RP X-RAY CRYSTALLOGRAPHY (1.5 ANGSTROMS).
RX MEDLINE=98181012; PubMed=9514739;
RA Papageorgiou A.C., Tranter H.S., Acharya K.R.;
RT "Crystal structure of microbial superantigen staphylococcal
RT enterotoxin B at 1.5-A resolution: Implications for superantigen
RT recognition by MHC class II molecules and T-cell receptors.";
RL J. Mol. Biol. 277:61-79(1998).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- DISEASE: STAPHYLOCOCCAL ENTEROTOXINS CAUSE THE INTOXICATION
CC STAPHYLOCOCCAL FOOD POISONING SYNDROME.
CC -1- SIMILARITY: BELONGS TO THE STAPHYLOCOCCAL/STREPTOCOCCAL TOXIN
CC FAMILY.
CC
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EMBL: M1118; AAC88550.1; ..

PIR: A01815; ENSAB6.

PIR: S27360; S27360.

PDB: 1SEB; 20-JUN-96.

PDB: 2SEB; 28-JAN-98.

PDB: 3SEB; 27-MAY-98.

PDB: 1SE3; 16-JUN-97.

PDB: 1SE4; 15-OCT-97.

PDB: 1SEB; 04-MAR-99.

InterPro: IPR001961; Staph/Strep_toxin.

Pfam: PF01123; Staph_Strp_toxin; 1.

Pfam: PF02876; Staph_Strp_tox_C; 1.

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DR PRINTS: PR00279; BACTRITOXIN.
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
KW Enterotoxin; Toxin; Signal; Superantigen; 3D-structure.
FT SIGNAL 1 27
FT CHAIN 28 266
FT DISULFID 120 140
FT CONFLICT 56 58
FT CONFLICT 69 77
FT CONFLICT 118 118
FT CONFLICT 128 130
FT CONFLICT 133 135
FT CONFLICT 149 150
FT CONFLICT 156 156
FT CONFLICT 185 186
FT CONFLICT 233 233
FT CONFLICT 246 247
SQ SEQUENCE 266 AA; B6D417F61CF018B0 CRC64;

Query Match 13.5%; Score 162.5; DB 1; Length 266;
Best Local Similarity 25.4%; Pred. No. 5.3e-06;
Matches 57; Conservative 40; Mismatches 86; Indels 41; Gaps 9;

QY 28 DNSSLRLNIYTIYVEYSDIVDFKT---SHNLVTKKLDVRDARDFINSEMEYAAAND 83
Db 57 DNHVSALNVKSIDQFLFDLIYSIKDKLGNIDNVRVEFFKNKLDADKYKDYVDFGANY 116
QY 84 F-----KTGDKIAVFSVPFDNLYSKGKVTAYTYGKITPYKTSIPK--NIPVNLWIN 134
Db 117 YQCYFSEKKN-----DINSHGTDKRTCKMYGVTGHEHNGNQLDKYSIRVFEED 166
QY 135 GKQISVPYNEISNKTVTQAQIDKLVKRLIAHQHLYS-SGSSYKSGRLVFTNDNSDK 193
Db 167 GKNLL--SFDVQTKKRVTAQELDYLRLVLYKKNKLYEFNNSPYETGYKFIENSEFW 224
QY 194 YSF-----DLFYVGYRDKESIFKVKYKDKNSFNIDKIGHLDIEID 232
Db 225 YDMPAPGDKF-----DQSKYLMYNDNK-----MVDSDKVKIE 258

RESULT 9
ETXG_STAAH
ID ETXG_STAAH STANDARD; PRT; 258 AA.
AC O85382;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DE Enterotoxin type G precursor (SEG).
GN ENTG OR SEG OR SAV1824 OR SA1642.
OS Staphylococcus aureus (strain Mu50 / ATCC 700699),
OS Staphylococcus aureus (strain N315), and
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=158878, 158879, 1280;
RN [1]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC STRAIN=FR1572;
RA MEDLINE=98298056; PubMed=9632603;
RA Munson S.H., Tremaine M.T., Welch M.J., Welch R.A.;
RT "Identification and characterization of staphylococcal enterotoxin
RT types G and I from Staphylococcus aureus.";
RL Infect. Immun. 66:3337-3348(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Mu50 / ATCC 700699, and N315;
RX MEDLINE=21311952; PubMed=11418146;
RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-Q., Ito T.,
RA Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,
RA Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
RA Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
RA Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
RA Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;

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RT "Whole genome sequencing of methicillin-resistant Staphylococcus
RT aureus.";
RL Lancet 357:1225-1240(2001).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- DISEASE: STAPHYLOCOCCAL ENTEROTOXINS CAUSE THE INTOXICATION
CC -1- STAPHYLOCOCCAL FOOD POISONING SYNDROME.
CC -1- SIMILARITY: BELONGS TO THE STAPHYLOCOCCAL/STREPTOCOCCAL TOXIN
CC FAMILY.
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CC -----
DR EMBL; AF064773; AAC26660.1; -
DR EMBL; AP003363; BAB57986.1; -
DR EMBL; AP003135; BAB42910.1; -
DR HSP; P01552; ISBB.
DR InterPro; IPR001961; Staph_Strep_toxin.
DR Pfam; PF01123; Staph_Strep_toxin; 1.
DR Pfam; PF02876; Staph_Strep_toxin; 1.
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; FALSE_NEG.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
KW Enterotoxin; Toxin; Signal; Superantigen; Complete proteome.
FT SIGNAL 1 25
FT CHAIN 26 258 ENTEROTOXIN TYPE G.
FT DISULFID 116 133 BY SIMILARITY.
SQ SEQUENCE 258 AA; E2982101701D012C CRC64;

Query Match 13.3%; Score 161; DB 1; Length 258;
Best Local Similarity 28.9%; Pred. No. 6.7e-06;
Matches 63; Conservative 43; Mismatches 62; Indels 50; Gaps 15;

QY 19 SRPVEGLEVDNLSRLNIYTIYVEYSDIV--IDFKTSHNLVTKKLDVRDARDFINSEM 76
Db 56 SPVVEG-----RGVINSRQLSHDLTFPIEVK-SYNEVKTELE-----NTEL 96
QY 77 DEYAANDFKTGDKIAVFSVPFDNLYL---SKGKVT-----AYTYGGIT-PYKTSIPKNI 127
Db 97 -----ANNYK-DKKVDIFGVPIFYTCIIPKSEPDINQNGCCMYGLTFFNSENERDKLI 151
QY 128 PVNLWINGKQISVPYNEISNKTVTQAQIDKLVKRLIAHQHLYS-SGSSYKSGRLVFEH 186
Db 152 TVQVTIDNRQ-SLGFT-ITTKNNWVTIQELDYKARHHLTKKKLYEPDGFSAFSGYIKF- 208
QY 187 TNDNSDKYSFDLF-----YGYRDKESIFKVKYKDKN 217
Db 209 TEKNNTSFWFDLPKPKELVPFVPYK---FLNIYGDNK 242

RESULT 10
ETC2_STAAU
ID ETC2_STAAU STANDARD; PRT; 266 AA.
AC P34071;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Enterotoxin type C-2 precursor (SEC2).
GN ENTC2.
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 28-66.
RX MEDLINE=89277549; PubMed=2543637;
RA Bohach G.A., Schlievert P.M.;
RT "Conservation of the biologically active portions of staphylococcal
RT enterotoxins C1 and C2.";
RL Infect. Immun. 57:2249-2252(1989).
RN [2]

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FT CHAIN 28 266 ENTEROTOXIN TYPE C-3.
FT DISULFID 120 137
SQ SEQUENCE 266 AA; 5ED8A32D11FFCA59 CRC64;

Query Match 12.9%; Score 156; DB 1; Length 266;
Best Local Similarity 26.1%; Pred. No. 1.7e-05;
Matches 54; Conservative 42; Mismatches 63; Indels 48; Gaps

Qy 40 IVYEYSDIVIDFKTSHNLVTKKIDVRDARDFINSEMDYAAAN-----DFKTGDKIAVFS 94
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 76 LIYNISDKKL--KNYDKVKTELLNEDLAKKYKDEVVDYVGSYYVNCYFSSKDNV---- 128
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

Qy 95 VPFQWNLVSGKVT---AYYGGITPVQKTSIP-----KNIPVNLWINGKQISVYPYNEIST 147
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 129 -----GKVTGGKTCMYGGITKTHGHNHFNGNLQNVLVRYVEN-KRNTISF-EVQT 176
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

Qy 148 NKTWTVAQIEDLKVRRFLIAQHOLYSSGSS-YKSGRLVVEHTDNS-----DKYS 195
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 177 DKSVTAQIEDIKARNEFLINKKLYEFNSSPYETGYIKFIENNGTFTWDMMPAPGDKFD 236
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

Qy 196 FDLFVGYGRDKESIFKYVKDKNSFNID 222
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 237 QSKYLMYNDNKTV-----DSKSVKIE 258
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 12
ETC1_STAAU STANDARD; PRT; 266 AA.
ID ETC1_STAAU STANDARD; PRT; 266 AA.
AC P01533;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 13-JUN-2002 (Rel. 41, Last annotation update)
DE Enterotoxin type c-1 precursor (SECI).
GN ENTC1.
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcaceae.
OX NCBI_TaxID=1280;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88038352; PubMed=28233067;
RA Bohach G.A., Schlievert P.M.;
RT "Nucleotide sequence of the staphylococcal enterotoxin C1 gene and
RL relatedness to other pyrogenic toxins.";
RM Mol. Gen. Genet. 209:15-20(1987).
RN [2]
RP SEQUENCE OF 28-266.
RX MEDLINE=83213327; PubMed=6189824;
RA Schmidt J.J., Spero L.;
RT "The complete amino acid sequence of staphylococcal enterotoxin C1.";
RJ J. Biol. Chem. 258:6300-6306(1983).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- DISEASE: STAPHYLOCOCCAL ENTEROTOXINS CAUSE THE INTOXICATION
CC STAPHYLOCOCCAL FOOD POISONING SYNDROME.
CC -1- SIMILARITY: BELONGS TO THE STAPHYLOCOCCAL/STREPTOCOCCAL TOXIN
CC FAMILY.
CC
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CC
CC EMBL; X05815; CA29260.1; -.
CC PIR; A01816; ENSACL.
CC PIR; S06356; S06356.
CC HSSP; P34071; 1SE2.
CC InterPro; IPR001961; Staph_Strep_toxin.
CC Pfam; PF01123; Staph_Strep_toxin; 1.
CC Pfam; PF02876; Staph_Strep_toxin; 1.
CC PRINTS; PS00279; BACTRLTOXIN.
CC PROSITE; PS00377; STAPH_STREP_TOXIN_1; 1.

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RP X-RAY CRYSTALLOGRAPHY (2.05 ANGSTROMS).
RX MEDLINE-97337442; PubMed-9194182;
RA Prasad G.S., Radhakrishnan R., Mitchell D.T., Earhart C.A.,
RA Dinges M.M., Cook W.J., Schlivert P.M., Ohlendorf D.H.,
RT "Refined structures of three crystal forms of toxic shock syndrome
RL toxin-1 and of a tetramutant with reduced activity.";
RN Protein Sci. 6:1220-1227(1997).
[6]
RP X-RAY CRYSTALLOGRAPHY (1.95 ANGSTROMS) OF MUTANTS.
RX MEDLINE-98254504; PubMed-9585531;
RA Earhart C.A., Mitchell D.T., Murray D.L., Pinheiro D.M., Matsumura M.,
RA Schlievert P.M., Ohlendorf D.H.,
RT "Structures of five mutants of toxic shock syndrome toxin-1 with
RT reduced biological activity.";
RL Biochemistry 37:7194-7202(1998).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- DISEASE: THIS TOXIN IS RESPONSIBLE FOR THE SYMPTOMS OF TOXIC
CC SHOCK SYNDROME.
CC -1- SIMILARITY: BELONGS TO THE STAPHYLOCOCCAL/STREPTOCOCCAL TOXIN
CC FAMILY.
CC
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CC
DR EMBL; J02615; AAA26682.1; -
DR PIR; A24606; XCSASI.
DR PDB; 2TSS; 24-DEC-97.
DR PDB; 3TSS; 24-DEC-97.
DR PDB; 4TSS; 24-DEC-97.
DR PDB; 5TSS; 24-DEC-97.
DR PDB; 1Q1L; 12-AUG-97.
DR PDB; 2Q1L; 12-AUG-97.
DR PDB; 1AW7; 18-NOV-98.
DR PDB; 1TS2; 16-DEC-98.
DR PDB; 1TS3; 16-DEC-98.
DR PDB; 1TS4; 16-DEC-98.
DR PDB; 1TS5; 16-DEC-98.
DR InterPro; IPR001961; Staph/Strep_toxin.
DR InterPro; IPR003999; Staph_toxin.
DR Pfam; PF01123; Staph_strip_toxin; 1.
DR Pfam; PF02876; Staph_strip_tox.C; 1.
DR PRINTS; PR01501; TOXICSSTOXIN.
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; FALSE_NEG.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
KW Toxin; Superantigen; Signal; 3D-structure.
FT SIGNAL 1 40
FT CHAIN 41 234 TOXIC SHOCK SYNDROME TOXIN-1.
SQ SEQUENCE 234 AA; 26306 MW; E95789FF9A1D7AB4 CRC64;
Query Match 9.3%; Score 112.5; DB 1; Length 234;
Best Local Similarity 21.1%; Pred. No. 0.041;
Matches 53; Conservative 35; Mismatches 98; Indels 65; Gaps 9;
QY 29 NNSLLRNIYTIYVESDIVDFK-----TSHNLV-TKKLDVRD-----ARDFFI 72
DB 2 NKLLMFFIVSPLLATTATDFTVPVLSNQIIRKAKASTNDIKDLWDYSSGSDTET 61
QY 73 NSEV-----DEVAANDKTDGKIAVFSVPFDKN-----Y 101
DB 62 NSEVLNLSGMRIRKIKTDGSGISLIIPSPYSPAFKGEKV-----DUNTRTKKSOH 114
QY 102 LSKGKVATYTGGITPYQKTSIPKNIPVNLWINGKOISYPYNEISTKTTVTAQEIIDLKV 161
DB 115 TSEGYTHFQISGVNTKLTPTLEPLKVKVHGKDSPLKYGK-KFDKQKLAISTLDLFEI 173
QY 162 RKFLIAHQIYSSGSSYKSRVFNHNDNSDKYSFDLFYVGYRDKESIFKVKYDNKNSFNI 221
DB 174 RHLQTOIHGLYR--SSDKTGGYWKITMNDGSTYQSOL-----SKKFEYNTKPPINI 223

QY 222 DKIGHLDIED 232
DB 224 DEIKTIEAEIN 234
RESULT 14
YKKL-CAEEL
ID YKKL-CAEEL STANDARD; PRT; 1010 AA.
AC P34278;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Hypothetical protein C02F5.1 in chromosome III.
GN C02F5.1
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Briscot N2;
RX MEDLINE-94150718; PubMed-7906398;
RA Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,
RA Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
RA Craxton M., Dear S., Du Z., Durbin R., Favello A., Fraser A.,
RA Fulton L., Gardner A., Green P., Hawkins T., Hillier L., Jier M.,
RA Johnston L., Jones M., Kershaw J., Kirsten J., Laister N.,
RA Letellier P., Lightning J., Lloyd C., Mortimore B., O'Callaghan M.,
RA Parsons J., Percy C., Rifkin L., Roopra A., Saunders D., Shownkeen R.,
RA Sims M., Smaldon N., Smith A., Smith M., Sonhammer E., Staden R.,
RA Sulston J., Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K.,
RA Waterston R., Watson A., Weinstein L., Wilkinson-Sproat J.,
RA Wohldman P.;
RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
RT elegans.";
RL Nature 368:32-38(1994).
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CC
DR EMBL; L14745; AAA27916.2; -
DR WormPep; C02F5.1; CE02450.
KW Hypothetical protein.
SQ SEQUENCE 1010 AA; 113231 MW; 15E19DD975824D94 CRC64;
Query Match 8.8%; Score 106.5; DB 1; Length 1010;
Best Local Similarity 22.0%; Pred. No. 0.73;
Matches 51; Conservative 48; Mismatches 90; Indels 43; Gaps 10;
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DB 213 ETNNVFNTLEAAEMDTS-----KLDENNTMNAIRIPINSNVMPVMDITEHHTLIBEK- 267
QY 63 DVRDARDFFINSEMDVAANDFKTGKIAVFSVPFDKNVLSKGVATYTGGITPYQKTS 122
DB 268 ----KNDTGPQLMISAPQVQVNDTLAIFNSPRD---ICNKL-----GV-PQLIN 313
QY 123 IPKN-TPVNLWINGKOISYPYNEISTKTTVTAQEIIDLKVKRFLIAHQIYSSGSSYKSG 181
DB 314 IASNVYPVDMIDITQAV---LNAEKNDQFETSQLMDSIPKVLV-----NDT 358
QY 182 RLVFHTNDNSDKYSFDLFYVGYRDKESIFKVKYDNKNSFNI-DKIGHLDIED 232
DB 359 MAMFNPKHVSKSSMDL-----EKTIEAANDKSTYPSIADVEYDLMDMD 403
RESULT 15

Search completed: February 14, 2003, 13:44:25
Job time : 14 secs

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OM protein - protein search, using sw model

Run on: February 14, 2003, 13:44:09 ; Search time 13 Seconds
(without alignments)
457.914 Million cell updates/sec

Title: US-09-869-136-2

Perfect score: 1207

Sequence: 1 MKKTKLIFSFTSIFIAISR.....KDNKSFNIDKIGHLDIEIDS 233

Scoring table:

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Gapop 10.0 , Gapext 0.5

Searched: 140259 seqs, 25548876 residues

Total number of hits satisfying chosen parameters: 140259

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications_AA.*

- 1: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pdb.*
- 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pdb.*
- 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pdb.*
- 4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pdb.*
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- 7: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pdb.*
- 8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pdb.*
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- 12: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pdb.*
- 13: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pdb.*
- 14: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pdb.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	255.5	21.2	257	US-09-870-759-8	Sequence 8, Appl
2	251	20.8	248	US-09-870-759-16	Sequence 16, Appl
3	251	20.8	258	US-09-870-759-14	Sequence 14, Appl
4	239.5	19.8	257	US-08-882-431-2	Sequence 2, Appl
5	231.5	19.2	233	US-08-882-431-4	Sequence 4, Appl
6	195.5	16.2	251	US-08-882-431-16	Sequence 16, Appl
7	195.5	16.2	251	US-08-882-431-13	Sequence 13, Appl
8	167.5	13.9	239	US-08-882-431-10	Sequence 10, Appl
9	162.5	13.5	239	US-09-150-947B-12	Sequence 12, Appl
10	162.5	13.5	266	US-09-870-759-10	Sequence 10, Appl
11	153.5	12.7	266	US-08-882-431-14	Sequence 14, Appl
12	153.5	12.7	266	US-08-882-431-12	Sequence 12, Appl
13	132.5	12.6	265	US-09-870-759-12	Sequence 8, Appl
14	148.5	12.3	265	US-08-882-431-6	Sequence 6, Appl
15	122	10.1	250	US-09-870-759-20	Sequence 20, Appl
16	112.5	9.3	234	US-09-870-759-18	Sequence 18, Appl
17	111	9.2	233	US-08-882-431-12	Sequence 12, Appl
18	96.5	8.0	226	US-09-815-242-5900	Sequence 5900, Ap
19	96.5	8.0	226	US-09-815-242-13156	Sequence 13156, A

20	87.5	7.2	451	9	US-09-910-186A-12	Sequence 12, Appl
21	84.5	7.0	445	10	US-09-815-242-5010	Sequence 5010, Ap
22	84.5	7.0	447	10	US-09-815-242-10908	Sequence 10908, A
23	84.5	7.0	951	9	US-09-924-097-15	Sequence 15, Appl
24	83.5	6.9	362	9	US-09-839-894-31	Sequence 31, Appl
25	82.5	6.8	539	9	US-09-738-626-6722	Sequence 6722, Ap
26	82.5	6.8	788	9	US-09-908-193-35	Sequence 35, Appl
27	82.5	6.8	818	9	US-10-055-364-44	Sequence 44, Appl
28	82	6.8	664	12	US-10-067-385-6	Sequence 6, Appl
29	82	6.8	1007	10	US-09-765-272-216	Sequence 216, App
30	82	6.8	1049	9	US-09-978-295A-496	Sequence 496, App
31	82	6.8	1049	9	US-09-978-697-496	Sequence 496, App
32	82	6.8	1049	9	US-09-978-192A-496	Sequence 496, App
33	82	6.8	1049	9	US-09-999-832A-496	Sequence 496, App
34	82	6.8	1049	9	US-09-978-189-496	Sequence 496, App
35	82	6.8	1049	9	US-10-028-072-358	Sequence 358, App
36	82	6.8	1049	9	US-10-121-049-358	Sequence 358, App
37	82	6.8	1049	9	US-10-123-904-358	Sequence 358, App
38	82	6.8	1049	9	US-10-140-470-358	Sequence 358, App
39	82	6.8	1049	9	US-10-095-627-1	Sequence 1, Appl
40	82	6.8	1049	9	US-10-175-746-358	Sequence 358, App
41	82	6.8	1049	9	US-10-176-918-358	Sequence 358, App
42	82	6.8	1049	9	US-10-176-921-358	Sequence 358, App
43	81.5	6.8	463	9	US-09-816-467-2	Sequence 2, Appl
44	81	6.7	359	9	US-09-839-894-29	Sequence 29, Appl
45	79	6.5	619	10	US-09-801-368-88	Sequence 88, Appl

ALIGNMENTS

RESULT 1
US-09-870-759-8
; Sequence 8, Application US/09870759
; Patent No. US20020177551A1
; GENERAL INFORMATION:
; APPLICANT: TERMAN, David S
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASES.
; FILE REFERENCE: 870759
; CURRENT APPLICATION NUMBER: US/09/870,759
; CURRENT FILING DATE: 2002-01-14
; PRIOR APPLICATION NUMBER: US 60/208,128
; PRIOR FILING DATE: 2000-05-30
; NUMBER OF SEQ ID NOS: 166
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 257
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-870-759-8

Query Match 21.2%; Score 255.5; DB 9; Length 257;
Best Local Similarity 29.9%; Pred. No. 1.8e-16;
Matches 58; Conservative 41; Mismatches 58; Indels 37; Gaps 7;

QY	44	YSDIVIDFKTSHNLVTKKLDVRDARDFEINSEMDVAANDFKTGDKIAVFSVPFQWNYLS	103
DB	88	YNDLLVDF-----DSKDIVDKYKGVLDYAY-----IGYOC	120
QY	104	KG---KVTAYTGGITPYQKTSI--PKNIPVNLWINGKOISYPYNEISTNKTVTVAQEID	158
DB	121	AGGTPNKTACMYGGVTLHDNNRLTEKKVPINLWLDGKQNTVPLETVTKNKNVQVQELD	180
QY	159	LKVRFLTAQHOLYSS---GSSYKSGRLVFTHTNDNSDKYSFOLFVYGVYRDKSIFKYKQ	215
DB	181	LOARYLQEKYLNYSVDVPGKVGQGLIVFHTS-TEPSYNYDLFGAQGQNSNTLLRIYRD	239
QY	216	NKSENIIDKIGHDI	229
DB	240	NKTINSENH-HIDI	252

RESULT 2

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US-09-870-759-16
; Sequence 16, Application US/09870759
; Patent No. US20020177551A1
; GENERAL INFORMATION:
; APPLICANT: TERMAN, David S
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
; FILE REFERENCE: 870759
; CURRENT APPLICATION NUMBER: US/09/870,759
; CURRENT FILING DATE: 2002-01-14
; PRIOR APPLICATION NUMBER: US 60/208,128
; PRIOR FILING DATE: 2000-05-30
; NUMBER OF SEQ. ID NOS: 166
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 16
; LENGTH: 248
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-870-759-16

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Query Match 20.8%; Score 251; DB 9; Length 248;
Best Local Similarity 26.3%; Pred. NO. 4.6e-16;
Matches 73; Conservative 53; Mismatches 67; Indels 86; Gaps 12;

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			:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:																								
Db	1	MKKT	A	F	I	L	-----	L	L	F	I	A	L	T	T	S	P	L	V	N	G	S	E	K	S	E	I	N	E	K	D	L	R	K	K	S	E	L	Q	R	N	A	L	S	L	R	O	I	Y	N	Y	-----	57		
Qy	38																																																						
Db	58	EK	A	I	T	E	N	K	S	D	D	O	F	L	E	N	T	L	L	F	G	F	F	T	G	H	P	W	N	D	L	L	V	-----	L	G	S	K	D	A	N	K	Y	K	G	-----	106								
Qy	74	S	E	M	D	E	Y	A	A	N	D	F	K	T	G	I	A	V	S	P	V	D	W	N	Y	L	S	K	-----	K	V	T	A	Y	T	Y	G	G	I	T	P	Y	Q	K	T	S	-----	128							
Db	107	K	Y	D	L	X	G	A	Y	-----																																													
Qy	129	V	N	L	I	N	G	K	O	I	S	P	Y	N	E	I	S	T	N	K	T	T	V	T	A	O	E	D	L	K	V	R	F	L	I	A	O	H	O	L	Y	S	-----	G	S	S	Y	K	S	G	R	L	V	-----	185
Db	151	I	N	L	I	D	G	K	T	T	P	I	D	K	V	S	K	K	E	V	T	V	O	E	L	D	L	O	A	R	Y	L	H	G	K	F	G	L	I	N	S	D	S	F	G	K	V	Q	R	L	V	-----	210		
Qy	186	H	T	N	D	N	S	D	K	Y	S	F	D	L	F	Y	G	Y	R	D	K	S	I	F	K	Y	K	D	N	K	S	F	N	I	D	K	I	-----	224																
Db	211	H	S	E	G	S	-----	T	W	S	D	L	F	A	Q	G	O	Y	P	T	L	I	A	R	I	Y	R	D	N	K	T	I	N	S																					

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RESULT 3
US-09-870-759-14
; Sequence 14, Application US/09870759
; Patent No. US20020177551A1
; GENERAL INFORMATION:
; APPLICANT: TERMAN, David S
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
; FILE REFERENCE: 870759
; CURRENT APPLICATION NUMBER: US/09/870,759
; CURRENT FILING DATE: 2002-01-14
; PRIOR APPLICATION NUMBER: US 60/208,128
; PRIOR FILING DATE: 2000-05-30
; NUMBER OF SEQ ID NOS: 166
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 14
; LENGTH: 258
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-870-759-14

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Query Match 20.8%; Score 251; DB 9; Length 258;
Best Local Similarity 29.4%; Pred. No. 4.8e-16;
Matches 77; Conservative 57; Mismatches 86; Indels 42; Gaps 13;

QY	1 MKKTKLIFS--F*SFIAIISRPFVGLVDNN-----SLLRNIYSTIVVEY 44 : : : : : : :
Db	1 MKKENILALAFF*SLVISPLN----VKANENIDSVKEKLHKKSLSSTALNNKKISY 55
QY	45 SD---IVIDEKTS-----HNLVTKKL--DVRDAROFFINSEMDVEYAANDFKTGDKIAVF 93

[illegible]

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RESULT 4
US-08-882-431-2
; Sequence 2, Application US/08882431
; Publication No. US2003009015A1
; GENERAL INFORMATION:
; APPLICANT: Robert G. Ulrich,
; APPLICANT: Mark A. Olson
; APPLICANT: Sina Bavari
; TITLE OF INVENTION: Bacterial Superantigen
; TITLE OF INVENTION: Vaccines
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: John Moran
; STREET: US Army MPMC -504 Scott Street MCMR-JA (John Moran-Patent Att'y)
; CITY: FORT DETRICK
; STATE: MARYLAND
; COUNTRY: USA
; ZIP: 21702-5012
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.5
; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/882,431
; FILING DATE: June 25, 1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Moran, John
; REGISTRATION NUMBER: 26,313
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 619-2065
; TELEFAX: (301) 619-7714
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 257
; TYPE: Amino Acid
; STRANDEDNESS: Unknown
; TOPOLOGY: Unknown
; MOLECULE TYPE: Peptide
; US-08-882-431-2

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Query Match          19.8%; Score 239.5; DB 1; Length 257;  
Best Local Similarity 29.4%; Pred. NO. 5.6e-15;  
Matches 57; Conservative 39; Mismatches 61; Indels 37; Gaps 7;  
  
QY      44 YSDIVDFKTSNHLVTKKLDVDRDARDFPFIENSEMDEYAANDFKTGDKTAVFSPFDWNYLS 103  
       |:::||| ::|| ::||| ::|||  
Db       88 YNDLLVR-----DSKDIDVKYKGKVDLYGAYA-----GYQC 120  
  
QY     104 KG---KVATYTYGGITPYQKTSI--PKNIPIVNLIWGKQISVPYNELSTNKTVTAQEID 158  
       ||||||| ::||| ::||| ::||| ::||| ::|||  
Db     121 AGGTFNRKTACMGCVTLHDNNRLETEKKVIPINLWDGKNQTVPLETVKTKNKNNTVOELD 180
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Qy 159 LKVRKFLIAQHLYSS---GSSYKSGRLVFTHTNDNSDKYSFDLFYVGYRDKESIFKVKYKD 215
 Db 181 LQARYLQEKYLNLYNSVDGVRQGLIVFHTS--TEPSVNYDLFGAQGOYSNTLLRIYRD 239
 Qy 216 NKSFNIDKIGHLDI 229
 Db 240 NKTINSENN-HIDI 252

RESULT 5
 US-08-882-431-4
 ; Sequence 4, Application US/08882431
 ; Publication No. US20030009015A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Robert G. Ulrich,
 ; APPLICANT: Mark A. Olson
 ; APPLICANT: Sina Bavari
 ; TITLE OF INVENTION: Bacterial Superantigen
 ; TITLE OF INVENTION: Vaccines
 ; NUMBER OF SEQUENCES: 16
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: John Moran
 ; STREET: US Army MRC -504 Scott Street MCMR-JA (John Moran-Patent Atty)
 ; CITY: FORT DETRICK
 ; STATE: MARYLAND
 ; COUNTRY: USA
 ; ZIP: 21702-5012
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: Apple Macintosh
 ; OPERATING SYSTEM: Macintosh 7.5
 ; SOFTWARE: Microsoft Word 6.0
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/882,431
 ; FILING DATE: June 25, 1997
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER:
 ; FILING DATE:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Moran, John
 ; REGISTRATION NUMBER: 26,313
 ; REFERENCE/DOCKET NUMBER:
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (301) 619-2065
 ; TELEFAX: (301) 619-7714
 ; INFORMATION FOR SEQ ID NO: 4:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 233
 ; TYPE: Amino Acid
 ; STRANDEDNESS: Unknown
 ; TOPOLOGY: Unknown
 ; MOLECULE TYPE: Peptide
 ; US-08-882-431-4

Query Match 19.2%; Score 231.5; DB 1; Length 233;
 Best Local Similarity 28.9%; Pred. No. 2.7e-14;
 Matches 56; Conservative 38; Mismatches 63; Indels 37; Gaps 7;
 Qy 44 YSDIVDFKTSNLTVKKLDVRDARDFINSEMDYAAANDFKTGDKIAVFSVPEDWNLYS 103
 Db 64 YNDLVRF-----DSKDIVDYKGGKVDLYGAYA-----GYQC 96
 Qy 104 KG---KVATYTGITPYQKTSI--PNKIPVNLWNGKQISVPYNEISTNKTVTYTAQID 158
 Db 97 AGGTPNKTACMYGGVTLHDNRLTEERKVPINLWLDGKQNTVPLETVKTNKKNVTQVDEL 156
 Qy 159 LKVRKFLIAQHLYSS---GSSYKSGRLVFTHTNDNSDKYSFDLFYVGYRDKESIFKVKYKD 215
 Db 157 KQARYLQEKYLNLYNSVDGVRQGLIVFHTS--TEPSVNYDLFGAQGOYSNTLLRIYRD 215
 Qy 216 NKSFNIDKIGHLDI 229

Db 216 NKTINSENN-HIDI 228
 RESULT 6
 US-08-882-431-16
 ; Sequence 16, Application US/08882431
 ; Publication No. US20030009015A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Robert G. Ulrich,
 ; APPLICANT: Mark A. Olson
 ; APPLICANT: Sina Bavari
 ; TITLE OF INVENTION: Bacterial Superantigen
 ; TITLE OF INVENTION: Vaccines
 ; NUMBER OF SEQUENCES: 16
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: John Moran
 ; STREET: US Army MRC -504 Scott Street MCMR-JA (John Moran-Patent Atty)
 ; CITY: FORT DETRICK
 ; STATE: MARYLAND
 ; COUNTRY: USA
 ; ZIP: 21702-5012
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: Apple Macintosh
 ; OPERATING SYSTEM: Macintosh 7.5
 ; SOFTWARE: Microsoft Word 6.0
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/882,431
 ; FILING DATE: June 25, 1997
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER:
 ; FILING DATE:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Moran, John
 ; REGISTRATION NUMBER: 26,313
 ; REFERENCE/DOCKET NUMBER:
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (301) 619-2065
 ; TELEFAX: (301) 619-7714
 ; INFORMATION FOR SEQ ID NO: 16:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 251
 ; TYPE: Amino Acid
 ; STRANDEDNESS: Unknown
 ; TOPOLOGY: Unknown
 ; MOLECULE TYPE: Peptide
 ; US-08-882-431-16

Query Match 16.2%; Score 195.5; DB 1; Length 251;
 Best Local Similarity 29.8%; Pred. No. 6.5e-11;
 Matches 73; Conservative 48; Mismatches 79; Indels 45; Gaps 16;
 Qy 5 KLIFSFTSIFTAI-ISRPVFG-----LEVNNLSLRNIYST-IVYEYSDIV-----ID 50
 Db 10 KMVFVLVTFGLTISQEVFAQQDDPSQLHRSSLVKLNQNIYFLYEGDPYTHENKVSVD 69
 Qy 51 FKTSHNLVTK-----KLDVRDARDFINSEMDYAAANDFKTGDK-IAVFSVP-FDW 99
 Db 70 QLRSHDLIYVSGPNYDKLKTCLK-----NQEM-----ATLEK--DKNVDIYGYEYVHL 116
 Qy 100 NYL-SKGKVTATYTGITPYO--KTSIPKIPVNLWNGKQISVPYNEISTNKTVTYTAQ 156
 Db 117 CYLCENAEARSACIYGGVTNHGEGNHLIETPKKIIVKVSIDGQI-SLSF-DIETNKKMVTAE 174
 Qy 157 IDLKVRFELIAQHLYSSG--SSYKSGRLVFTHTNDNSDKYSFDLFYVGYRDKESIFKVKYKD 215
 Db 175 LDYKVRKYLTDNKOLYTNGPSKYETGIKF-IPKNKESFWDFDFPEPEFTQSKYLMYKD 233
 Qy 216 NKSFN 220
 Db 234 NETLD 238

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; OPERATING SYSTEM: Macintosh 7.5
; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA: US/08/882.431
; APPLICATION NUMBER: US/08/882.431
; FILING DATE: June 25, 1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Moran, John
; REGISTRATION NUMBER: 26,313
; REFERENCE/DOCKET NUMBER:
; TELEPHONE: (301) 619-2065
; TELEFAX: (301) 619-7714
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 239
; TYPE: Amino Acid
; STRANDEDNESS: Unknown
; TOPOLOGY: Unknown
; MOLECULE TYPE: Peptide
; US-08-882-431-10

Query Match 13.9% Score 167.5; DB 1; Length 239;
Best Local Similarity 25.7%; Pred. No. 2.4e-08;
Matches 57; Conservative 40; Mismatches 88; Indels 37; Gaps 9;

; QY 28 DNNLLRNIVYYSIDVIDPKT----SHNLVTKKLDVRDARDFINSEMEDEYAAND 83
; Db 30 DNHVSAINVKSIDQFRYFDLIYSKDTKLGNDVNRVVEFNKDLADKYKDYVDVFGAN- 88
; QY 84 FKTDKTAIVSVFP-----DNVYLSKGVTAITYGTTGYOKTIPK--NTPVNLWINGK 136
; Db 89 -----AYQCAFSSKKTNDINSHQDTRKRTCMYGVTEHNGNOLDKRYRSITVRFEDGK 141
; QY 137 QISVPVNEISFTNKTVTTAQETDLKVRFLIAQHOLYS-SGSSYKSGRLVHTNDNSDKYS 195
; Db 142 NLL--SFDVOTNKKVTAQELDYLRHLYKDKKLYEFNNSPYETGVIKFIENENSFWYD 199
; QY 196 F-----DLFYGVGRDKESIFKVKYDNKSNFNDIKIGHLDIETD 232
; Db 200 MPPAPGDKF-----DQSKYLMYNDNK-----WYDSKDVKIE 231

RESULT 9
US-09-150-947B-12
; Sequence 12, Application US/09150947B
; Patent No. US20020028211A1
; GENERAL INFORMATION:
; APPLICANT: Kaempfer, Raymond
; APPLICANT: Arad, Gila
; TITLE OF INVENTION: BROAD SPECTRUM PYROGENIC EXOTOXINS
; FILE REFERENCE: A31967-PCT-USA-A
; CURRENT APPLICATION NUMBER: US/09/150,947B
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: PCT/IL97/00438
; PRIOR FILING DATE: 1997-12-30
; PRIOR APPLICATION NUMBER: ISRAEL 119938
; PRIOR FILING DATE: 1996-12-30
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 12
; LENGTH: 239
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
; US-09-150-947B-12

Query Match 13.5% Score 162.5; DB 10; Length 239;
Best Local Similarity 25.4%; Pred. No. 6.9e-08;
Matches 57; Conservative 40; Mismatches 86; Indels 41; Gaps 9;

; QY 5 KLIFSETSIFAI-ISRPFVG-----LEVNNLLRNIVYST-IVVEYSIDV-----ID 50
; Db 10 KMFEVLVTFLGTISQEVFAQDPPQSLSLHRSLSLVKNLQNIYFLVGDPTVHNKVSVD 69
; QY 51 FKTSNHLVTK-----KLDVRDARDFINSEMEDEYAANDPKTDGK-TAVFSVP-FDW 99
; Db 70 QLLSHLLIYNVSGPNYDKLTELK-----NQEM-----ATLEK--DKNVDIYGVEXYHL 116
; QY 100 NYL-SKGKVTAYTGGTTPQ--KTSTPKNIPVNLWINGKQISVPYNEISTNKTVTTAQE 156
; Db 117 CYLCENARACIYGGVTNHEGHNLEIPKKIVVKVSDIGIQ-SLSF-DIETNKKWYTAQE 174
; QY 157 IDLKRKFLIAQHOLYS-SGSSYKSGRLVHTNDNSDKYSFDFYGVGRDKESIFKVKYKD 215
; Db 175 LDYKVRKYLTDNKLQNTNGSKYETGVIK-IPKNESFWDFEPPEFTQSKYLYMIYKD 233
; QY 216 NKSFN 220
; Db 234 NETLD 238

RESULT 8
US-08-882-431-10
; Sequence 10, Application US/08882431
; Publication No. US2003009015A1
; GENERAL INFORMATION:
; APPLICANT: Robert G. Ulrich,
; APPLICANT: Mark A. Olson
; APPLICANT: Sinda Bavari
; TITLE OF INVENTION: Bacterial Superantigen
; FILE REFERENCE: Vaccines
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: John Moran
; STREET: US Army MRCM -504 Scott Street MCMR-JA (John Moran-Patent Atty)
; CITY: FORT DETRICK
; STATE: MARYLAND
; COUNTRY: USA
; ZIP: 21702-5012
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
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QY 28 DNSSLRNITVIVEYSDIVDFKT-----SHNLVTKLDVRDARDFFINSEMDYAAND 83
 Db 30 DNHVSAINVKSIDQFLYDIYSIKDTKLGNDYDNRVFEKNDLADKYDKYVDFEGANY 89
 QY 84 F-----KTGDKIAVSPEDWNLKSKVTAITYGGITPYQKTSIPK--NIPVNLWIN 134
 Db 90 YQCYFESKTN-----DINSHETDKRKTCTMGVTEHNGNOLDKYSITVRVFD 139
 QY 135 GKQISVPYNEISTNKTVTVAEIDLKVRKFLIAQHOLYS--SGSSYSKGRVLVPHFTNDNSDK 193
 Db 140 GKNLL--SFDVQTNKKVTAQELDYLTRHYLVKNKKLYEFNNSPYETGYIKFIENENSW 197
 QY 194 YSF-----DLFVGVGRDKESIFKYVDKNSFNIDKIGHLDIEID 232
 Db 198 YDMPAPGDKF-----DQSKYLMYNDNK-----MYDSKDVKIE 231

RESULT 10

US-09-870-759-10
 ; Sequence 10, Application US/09870759
 ; Patent No. US20020177551A1
 ; GENERAL INFORMATION:
 ; APPLICANT: TERMAN, David S
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
 ; FILE REFERENCE: 870759
 ; CURRENT APPLICATION NUMBER: US/09/870,759
 ; CURRENT FILING DATE: 2002-01-14
 ; PRIOR APPLICATION NUMBER: US 60/208,128
 ; PRIOR FILING DATE: 2000-05-30
 ; NUMBER OF SEQ ID NOS: 166
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 10
 ; LENGTH: 266
 ; TYPE: PRT
 ; ORGANISM: Staphylococcus aureus
 US-09-870-759-10

Query Match 13.5%; Score 162.5; DB 9; Length 266;
 Best Local Similarity 25.4%; Pred. No. 8e-08;
 Matches 57; Conservative 40; Mismatches 86; Indels 41; Gaps 9;

QY 28 DNSSLRNITVIVEYSDIVDFKT-----SHNLVTKLDVRDARDFFINSEMDYAAND 83
 Db 57 DNHVSAINVKSIDQFLYDIYSIKDTKLGNDYDNRVFEKNDLADKYDKYVDFEGANY 116
 QY 84 F-----KTGDKIAVSPEDWNLKSKVTAITYGGITPYQKTSIPK--NIPVNLWIN 134
 Db 117 YQCYFESKTN-----DINSHOTDKRKTCTMGVTEHNGNOLDKYSITVRVFD 166
 QY 135 GKQISVPYNEISTNKTVTVAEIDLKVRKFLIAQHOLYS--SGSSYSKGRVLVPHFTNDNSDK 193
 Db 167 GKNLL--SFDVQTNKKVTAQELDYLTRHYLVKNKKLYEFNNSPYETGYIKFIENENSW 224
 QY 194 YSF-----DLFVGVGRDKESIFKYVDKNSFNIDKIGHLDIEID 232
 Db 225 YDMPAPGDKF-----DQSKYLMYNDNK-----MYDSKDVKIE 258

RESULT 11

US-08-882-431-14
 ; Sequence 14, Application US/08882431
 ; Publication No. US20030005015A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Robert G. Ulrich,
 ; APPLICANT: Mark A. Olson
 ; APPLICANT: Sina Bavari
 ; TITLE OF INVENTION: Bacterial Superantigen
 ; NUMBER OF SEQUENCES: 16
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: John Moran
 ; STREET: US Army MRC -504 Scott Street MCMR-JA (John Moran-Patent Atty)

CITY: FORT DETRICK
 STATE: MARYLAND
 COUNTRY: USA
 ZIP: 21702-5012
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: Apple Macintosh
 OPERATING SYSTEM: Macintosh 7.5
 SOFTWARE: Microsoft Word 6.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/882,431
 FILING DATE: June 25, 1997
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER:
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Moran, John
 REGISTRATION NUMBER: 26,313
 REFERENCE/DOCKET NUMBER:
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (301) 619-2065
 TELEFAX: (301) 619-7714
 INFORMATION FOR SEQ ID NO: 14:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 266
 TYPE: Amino Acid
 STRANDEDNESS: Unknown
 TOPOLOGY: Unknown
 MOLECULE TYPE: Peptide
 US-08-882-431-14

Query Match 12.7%; Score 153.5; DB 1; Length 266;
 Best Local Similarity 28.5%; Pred. No. 5.4e-07;
 Matches 55; Conservative 41; Mismatches 60; Indels 37; Gaps 12;

QY 55 HNLVTKLDVRDARDFFINSE--MDEYANDFTGKIAVSPVFDWN--YLSK---GKVT 108
 Db 78 YNISDKLKNYDK----VKTELLNGLAKYK-DEVVDYGSNYVYVNCYFSSKDNVGVKT 132
 QY 109 ---ATYGGITPYQKTSIP-----KNIPVNLWINGKQISVPYNEISTNKTVTVAEIDLKV 161
 Db 133 GKGTCMYGGITKHEGNHFNGLQNLVIRYEN-KRNTISF-EVOTDKKSVTAQELDIKA 190
 QY 162 RKFLIAQHOLYSGSS--YKSGRLVPHFTNDNS-----DKYSFDLPYGVGRDKESI 209
 Db 191 RNFLINKNLNLYEFNSFVETGYIKFIENNGNTFYDMPAPGDKFDQSKYLMYNDNRTV 250
 QY 210 FKVYKDNKSFNID 222
 Db 251 -----DSKSVKIE 258

RESULT 12

US-09-870-759-12
 ; Sequence 12, Application US/09870759
 ; Patent No. US20020177551A1
 ; GENERAL INFORMATION:
 ; APPLICANT: TERMAN, David S
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
 ; FILE REFERENCE: 870759
 ; CURRENT APPLICATION NUMBER: US/09/870,759
 ; CURRENT FILING DATE: 2002-01-14
 ; PRIOR APPLICATION NUMBER: US 60/208,128
 ; PRIOR FILING DATE: 2000-05-30
 ; NUMBER OF SEQ ID NOS: 166
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 12
 ; LENGTH: 266
 ; TYPE: PRT
 ; ORGANISM: Staphylococcus aureus
 US-09-870-759-12

[illegible]

Qy 140 VPEYNEISTNKTVAQEIQLKVRKELIAQHOLYS-SGSSYKSGRLVFTNDN----- 190
 Db 175 VOY-----NKKVTAQELDYLRHLYNKKLYEFNNSPYETGYIKFIENQNFWDMPA 229
 Qy 191 -SDKYSDFLFYGYRDKESIFKVKYKDNKSFNID 222
 Db 230 PGDKFAQSKYLMYNDNKMV-----DSKDVKLE 257

RESULT 15

US-09-870-759-20
 ; Sequence 20, Application US/09870759
 ; Patent No. US20020177551A1
 ; GENERAL INFORMATION:
 ; APPLICANT: TERMAN, David S
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
 ; FILE REFERENCE: 870759
 ; CURRENT APPLICATION NUMBER: US/09/870,759
 ; CURRENT FILING DATE: 2002-01-14
 ; PRIOR APPLICATION NUMBER: US 60/208,128
 ; PRIOR FILING DATE: 2000-05-30
 ; NUMBER OF SEQ ID NOS: 166
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 20
 ; LENGTH: 250
 ; TYPE: PRT
 ; ORGANISM: Streptococcus pyogenes
 US-09-870-759-20

Query Match 10.1%; Score 122; DB 9; Length 250;
 Best Local Similarity 27.7%; Pred. No. 0.00042;
 Matches 52; Conservative 32; Mismatches 70; Indels 34; Gaps 12;

Qy 49 IDFKTSHNLVTK-----KLDVRDARDFEINSEMDEYAANDPKGTGDK-IAVFSVP-F 97
 Db 68 VDQLSHDLIYNVSGPNVDKLTCLK-----NQEM----ATLEK--DKNVDIYGEY 114
 Qy 98 DWNYL-SKGKVTATYTGITPYQ--KTSIPKNIPVNLWINKQ-ISVPYNEISTNKTTVT 153
 Db 115 HLCYLCENAEASACLYGGVTNHEGNHLEIPKKIVKVSIDGTSLSFDIEQIKNG----N 170
 Qy 154 AQEIDLKVRFLIAQHOLYSSG-SYKSGRLVFTNDNSDKYSFDLFYVGYRDKESIFKV 212
 Db 171 CSRSIVYVRKYLTKNQLYNGPSKYETGYIKF-IPKNKESFWDFPFPEFTOSKYLMI 229
 Qy 213 YKDNKSFN 220
 Db 230 YKDNETLD 237

Search completed: February 14, 2003, 13:46:32
 Job time : 14 secs

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OM protein - protein search, using sw model

Run on: February 14, 2003, 13:44:04 ; Search time 36 Seconds

(without alignments)
862.428 Million cell updates/sec

Title: US-09-869-136-2

Perfect score: 1207

Sequence: 1 MKTKLIFSFTSIFALISR.....KDNKSFNIDKIGHLDIEIDS 233

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 2: /SID52/gcgdata/geneseq/geneseq-emb1/AA1981.DAT.*
- 3: /SID52/gcgdata/geneseq/geneseq-emb1/AA1982.DAT.*
- 4: /SID52/gcgdata/geneseq/geneseq-emb1/AA1983.DAT.*
- 5: /SID52/gcgdata/geneseq/geneseq-emb1/AA1984.DAT.*
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- 7: /SID52/gcgdata/geneseq/geneseq-emb1/AA1986.DAT.*
- 8: /SID52/gcgdata/geneseq/geneseq-emb1/AA1987.DAT.*
- 9: /SID52/gcgdata/geneseq/geneseq-emb1/AA1988.DAT.*
- 10: /SID52/gcgdata/geneseq/geneseq-emb1/AA1989.DAT.*
- 11: /SID52/gcgdata/geneseq/geneseq-emb1/AA1990.DAT.*
- 12: /SID52/gcgdata/geneseq/geneseq-emb1/AA1991.DAT.*
- 13: /SID52/gcgdata/geneseq/geneseq-emb1/AA1992.DAT.*
- 14: /SID52/gcgdata/geneseq/geneseq-emb1/AA1993.DAT.*
- 15: /SID52/gcgdata/geneseq/geneseq-emb1/AA1994.DAT.*
- 16: /SID52/gcgdata/geneseq/geneseq-emb1/AA1995.DAT.*
- 17: /SID52/gcgdata/geneseq/geneseq-emb1/AA1996.DAT.*
- 18: /SID52/gcgdata/geneseq/geneseq-emb1/AA1997.DAT.*
- 19: /SID52/gcgdata/geneseq/geneseq-emb1/AA1998.DAT.*
- 20: /SID52/gcgdata/geneseq/geneseq-emb1/AA1999.DAT.*
- 21: /SID52/gcgdata/geneseq/geneseq-emb1/AA2000.DAT.*
- 22: /SID52/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*
- 23: /SID52/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1207	100.0	233	21	AA193741 Amino acid sequenc
2	1126	93.3	258	23	ABP29565 Streptococcus poly
3	305	25.3	235	23	ABP29257 Streptococcus poly
4	297	24.6	235	19	AAW62787 Mutant streptococc
5	297	24.6	235	19	AAW62788 Mutant streptococc
6	296	24.5	235	19	AAW62784 Streptococcal pyro
7	285.5	23.7	208	12	AA13210 Streptococcus ent
8	285.5	23.7	208	14	AA13210 Streptococcus ent
9	285.5	23.7	208	22	AA13210 Streptococcus pyro
10	285.5	23.7	208	23	ABP76241 Staphylococcus pyo

11	274	22.7	235	19	AAW62785 Mutant streptococc
12	270	22.4	235	19	AAW62786 Mutant streptococc
13	259	21.5	232	23	ABP29143 Streptococcus poly
14	258.5	21.4	257	22	AAU14103 Peptide sequence f
15	256	21.2	230	22	AAW67339 Staphylococcus aur
16	256	21.2	245	18	AAW35374 Staphylococcus ent
17	252	20.9	245	18	AAW35375 Staphylococcus ent
18	251.5	20.8	233	18	AAW35373 Staphylococcus ent
19	251.5	20.8	233	18	AAW06738 Staphylococcus ent
20	251.5	20.8	257	22	AAU14104 Peptide sequence f
21	248.5	20.6	228	14	AAW5013 Staphylococcal ent
22	248.5	20.6	228	22	AAW67340 Staphylococcus aur
23	248.5	20.6	228	23	ABP76236 Staphylococcus aur
24	245.5	20.3	259	23	ABP29357 Streptococcus poly
25	244.5	20.3	233	14	AAW5011 Staphylococcal ent
26	244.5	20.3	233	22	AAW67338 Staphylococcus aur
27	243	20.1	234	21	AAW93742 Amino acid sequenc
28	241.5	20.0	233	23	ABP29092 Streptococcus poly
29	241.5	20.0	233	23	ABP76234 Staphylococcus aur
30	240.5	19.9	228	12	AA13205 Staphylococcal ent
31	239.5	19.8	233	21	AAW54463 Amino acid sequenc
32	239.5	19.8	233	23	ABP79502 Staphylococcal ent
33	239.5	19.8	257	21	AAW70102 Staphylococcal ent
34	239.5	19.8	257	23	ABP79501 Staphylococcal ent
35	234.5	19.4	233	12	AA13203 Staphylococcal ent
36	231.5	19.2	233	21	AAW70103 Mutant Staphylococ
37	228	18.9	230	12	AA13204 Staphylococcal ent
38	228	18.9	230	14	AAW5012 Staphylococcal ent
39	225	18.6	230	23	ABP76235 Staphylococcus aur
40	203	16.8	236	21	ABP29358 Amino acid sequenc
41	203	16.8	236	23	ABP29358 Streptococcus poly
42	200.5	16.6	251	18	AAW12153 Streptococcus pyog
43	200	16.6	250	18	AAW12145 Streptococcus pyog
44	199.5	16.5	251	18	AAW12151 Streptococcus pyog
45	196.5	16.3	251	18	AAW12146 Streptococcus pyog

ALIGNMENTS

RESULT 1
AA193741
ID AA193741 standard; Protein; 233 AA.
XX
AC AA193741;
XX
DT 03-OCT-2000 (first entry)
XX
DE Amino acid sequence of the mature SMEZ-2 superantigen protein.
XX
KW Sperantigen; SMEZ-2; SPE-G; SPE-H; SPE-J; Streptococcal disease;
KW Kawasaki syndrome; T cell activation; cancer therapy.
XX
OS Streptococcus pyogenes.
XX
PN WO200039159-A1.
XX
PD 06-JUL-2000.
XX
PF 24-DEC-1999; 99WO-N200228.
XX
PR 24-DEC-1998; 98NZ-0333589.
XX
FA (AUCC-) AUCCLAND UNISERVICES LTD.
XX
FI Fraser JD, Proft T;
XX
DR WPI; 2000-452370/39.
XX
N-PSDB; AAA47147.
XX
Novel superantigens from streptococcus pyogenes useful for genotyping
streptococcus pyogenes clones expressing SMEZ-2 and for diagnosing a
Kawasaki syndrome

XX PS Claim 2; Fig 2; 72pp; English.

CC The present sequence represents the SMEZ-2 superantigen protein. The

CC specification describes superantigen proteins SMEZ-2, SPE-G, SPE-H

CC and SPE-J. The superantigen polynucleotides and polypeptides are

CC used for subtyping Streptococci. They are also used for diagnosing

CC Streptococcal disease. The superantigens are used in diagnosis of

CC disease such as Kawasaki syndrome. They are also useful to recruit

CC and activate T cells in a relatively non-specific fashion since

CC they bind a large number of T cell receptor molecules by binding to the

CC Vbeta domain. Superantigen constructs are useful in cancer therapy.

XX Sequence 233 AA;

Query Match 100.0%; Score 1207; DB 21; Length 233;

Best Local Similarity 100.0%; Pred. No. 7.3e-101;

Matches 233; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKKTKLIFSFTSIFTAIISRVPFVGLVDNNSLLRNISYTIYVEYSDIVDFKTSNHLVTK 60

DB 1 MKKTKLIFSFTSIFTAIISRVPFVGLVDNNSLLRNISYTIYVEYSDIVDFKTSNHLVTK 60

QY 61 KLDVRDARDFFINSEMDEYAANDFKTGKIAVSPFDNVLKSGKVTAYTYGGTTPYOK 120

DB 61 KLDVRDARDFFINSEMDEYAANDFKTGKIAVSPFDNVLKSGKVTAYTYGGTTPYOK 120

QY 121 TSIPKNIPVNLWINGKQISVPYNEISTNKTVTTAQEIIDLKVRKFLIAHQHLYSSGSSYKS 180

DB 121 TSIPKNIPVNLWINGKQISVPYNEISTNKTVTTAQEIIDLKVRKFLIAHQHLYSSGSSYKS 180

QY 181 GRLVFHTNDNSDKYSFDLFYVGYRDKESIFKVKYKDNKSFNIDKIGHLDIEIDS 233

DB 181 GRLVFHTNDNSDKYSFDLFYVGYRDKESIFKVKYKDNKSFNIDKIGHLDIEIDS 233

RESULT 2

ABP29565

ID ABP29565 standard; Protein: 258 AA.

XX AC ABP29565;

XX DT 02-JUL-2002 (first entry)

XX DE Streptococcus polypeptide SEQ ID NO 8306.

XX KW Streptococcus; GAS; GBS; group B streptococcus; Streptococcus agalactiae;

XX KW group A streptococcus; Streptococcus pyogenes; antibacterial;

XX KW antinflammatory; infection; vaccine; meningitis; gene therapy.

XX OS Streptococcus pyogenes.

XX WO200234771-A2.

XX PD 02-MAY-2002.

XX PF 29-OCT-2001; 2001WO-GB04789.

XX PR 27-OCT-2000; 2000GB-0026333.

XX PR 24-NOV-2000; 2000GB-0028727.

XX PR 07-MAR-2001; 2001GB-0005640.

XX (CHIR-) CHIRON SPA.

XX (GENO-) INST GENOMIC RES.

XX Telford J, Masignani V, Margarit Ros YI, Grandi G, Fraser C;

XX Tetelin H;

XX WPI; 2002-352536/38.

XX N-PSDB; ABN70196.

XX New Streptococcus protein for the treatment or prevention of infection

XX or disease caused by Streptococcus bacteria, such as meningitis, and

PT for detecting a compound that binds to the protein -

XX Claim 1; Page 3947; 4525pp; English.

XX The invention relates to a protein (ABP25413-ABP30895) from group B

CC Streptococcus/GBS (Streptococcus agalactiae) or group A streptococcus/GAS

CC (Streptococcus pyogenes), comprising one of 5483 sequences (S1), given in

CC the specification. The proteins have antibacterial and antinflammatory

CC activity. (I), nucleic acids encoding (I), ABN66044-ABN71526 and

CC antibodies that bind (I) are used in the manufacture of medicaments for

CC the treatment or prevention of infection or disease caused by

CC Streptococcus bacteria, particularly S. agalactiae and S. pyogenes.

CC Nucleic acids encoding (I) are used to detect Streptococcus in a

CC biological sample. (I) is used to determine whether a compound binds to

CC (I). A composition comprising (I) or a nucleic acid encoding (I), may be

CC used as a vaccine or diagnostic composition. The disease caused by

CC Streptococcus that is prevented or treated may be meningitis. Nucleic

CC acid encoding (I) may be used to recombinantly produce (I) and may be

CC used in gene therapy. Antibodies to (I) are used for affinity

CC chromatography, immunoassays, and distinguishing/identifying

CC Streptococcus proteins.

XX Sequence 258 AA;

Query Match 93.3%; Score 1126; DB 23; Length 258;

Best Local Similarity 92.7%; Pred. No. 1.7e-93;

Matches 216; Conservative 8; Mismatches 9; Indels 0; Gaps 0;

QY 1 MKKTKLIFSFTSIFTAIISRVPFVGLVDNNSLLRNISYTIYVEYSDIVDFKTSNHLVTK 60

DB 26 MKKTKLIFSFTSIFTAIISRVPFVGLVDNNSLLRNISYTIYVEYSDIVDFKTSNHLVTK 85

QY 61 KLDVRDARDFFINSEMDEYAANDFKTGKIAVSPFDNVLKSGKVTAYTYGGTTPYOK 120

DB 86 KLDVRDARDFFINSEMDEYAANDFKTGKIAVSPFDNVLSECKVIATYTGMTPYOK 145

QY 121 TSIPKNIPVNLWINGKQISVPYNEISTNKTVTTAQEIIDLKVRKFLIAHQHLYSSGSSYKS 180

DB 146 EPMSKNIPVNLWINKQIPVPYINQISTNKTVTTAQEIIDLKVRKFLISQHLYSSGSSYKS 205

QY 181 GRLVFHTNDNSDKYSFDLFYVGYRDKESIFKVKYKDNKSFNIDKIGHLDIEIDS 233

DB 206 GRLVFHTNDNSDKYSFDLFYVGYRDKESIFKVKYKDNKSFNIDKIGHLDIEIDS 258

RESULT 3

ABP29257

ID ABP29257 standard; Protein: 235 AA.

XX AC ABP29257;

XX DT 02-JUL-2002 (first entry)

XX DE Streptococcus polypeptide SEQ ID NO 7690.

XX KW Streptococcus; GAS; GBS; group B streptococcus; Streptococcus agalactiae;

XX KW group A streptococcus; Streptococcus pyogenes; antibacterial;

XX KW antinflammatory; infection; vaccine; meningitis; gene therapy.

XX OS Streptococcus pyogenes.

XX WO200234771-A2.

XX PD 02-MAY-2002.

XX PF 29-OCT-2001; 2001WO-GB04789.

XX PR 27-OCT-2000; 2000GB-0026333.

XX PR 24-NOV-2000; 2000GB-0028727.

XX PR 07-MAR-2001; 2001GB-0005640.

XX (CHIR-) CHIRON SPA.

XX (GENO-) INST GENOMIC RES.

XX Telford J, Masignani V, Margarit Ros YI, Grandi G, Fraser C;
 PI Tettelein H;
 XX WPI; 2002-352536/38.
 DR N-PSDB; ABN69888.
 XX New Streptococcus protein for the treatment or prevention of infection
 PT or disease caused by Streptococcus bacteria, such as meningitis, and
 PT for detecting a compound that binds to the protein -
 XX
 PS Claim 1; Page 3906; 4525pp; English.
 XX The invention relates to a protein (ABP25413-ABP30895) from group B
 CC Streptococcus (Streptococcus agalactiae) or group A streptococcus/GAS
 CC (Streptococcus pyogenes), comprising one of 5483 sequences (S1), given in
 CC the specification. The proteins have antibacterial and antiinflammatory
 CC activity. (I), nucleic acids encoding (I), ABN6044-ABN71526 and
 CC antibodies that bind (I) are used in the manufacture of medicaments for
 CC the treatment or prevention of infection or disease caused by
 CC Streptococcus bacteria, particularly S. agalactiae and S. pyogenes.
 CC Nucleic acids encoding (I) are used to detect Streptococcus in a
 CC biological sample. (I) is used to determine whether a compound binds to
 CC (I). A composition comprising (I) or a nucleic acid encoding (I), may be
 CC used as a vaccine or diagnostic composition. The disease caused by
 CC Streptococcus that is prevented or treated may be meningitis. Nucleic
 CC acid encoding (I) may be used to recombinantly produce (I) and may be
 CC used in gene therapy. Antibodies to (I) are used for affinity
 CC chromatography, immunoassays, and distinguishing/identifying
 CC Streptococcus proteins.
 XX Sequence 235 AA;
 SQ
 Query Match 25.3%; Score 305; DB 23; Length 235;
 Best Local Similarity 32.7%; Pred. No. 1.5e-19;
 Matches 80; Conservative 45; Mismatches 96; Indels 24; Gaps 9;
 QY 1 MKK---TKLIFSTSFIAISRPPVGLVDNNSLLRNI-----YSTIVYEYSDIVID 50
 DB 1 MKKNIKIIVITVILISTIS-PI--IKSDSKDISNVKSDLLAYATTIPYDKNCRVN 57
 QY 51 FKTSH--NLVTKKLDVRDARDFINSEMDYEAANDFKTGDKIAVFSVPDWNLSKGVY 108
 DB 58 FSTTLNIDTKY---RGKDYIISSEMSYASQKPKRDHVDVGL----FYILNSHTG 110
 QY 109 AYTGGITPYQKTSIPKPNVNLWNGKQISVPYNEISTNTTVAQEDLKVKKFLIAQ 168
 DB 111 EYIGGITPAQNNKYNHKLGNLFISGESQQLNNKILIEKDIYVTFQEDFKIRKYLMDN 170
 QY 169 HOLYSSGSYKSGRLVHFHTNDNSKYSFDLF-YVGYRDKESIFKVKYDNKSNFIDKIGHL 227
 DB 171 KYIDATSPYVSGRIEIGTKDGKHE-QIDLFDPNENGRSDIFAKYKDNRIINMKNFHSF 229
 QY 228 DIEID 232
 DB 230 DYILE 234
 RESULT 4
 ID AAW62787 standard; Protein; 235 AA.
 XX AAW62787;
 XX AAW62787;
 XX 24-SEP-1998 (first entry)
 DE Mutant streptococcal pyrogenic exotoxin type C (SPE-C).
 KW Streptococcus pyrogenic exotoxin type C; SPE-C toxin; STSS;
 KW streptococcal toxic shock syndrome; mutant; vaccine.
 OS Streptococcus pyrogenes.
 XX

Key Location/Qualifiers
 1..27
 /note= "signal peptide"
 28..235
 /note= "mature protein"
 optionally substituted with Ala"
 Misc-difference 42
 /label= Y15A
 /note= "Tyr at position 15 of the mature protein
 substituted with Ala"
 Misc-difference 65
 /label= N38A
 /note= "Asn at position 38 of the mature protein
 substituted with Ala"
 WO9824910-A2.
 11-JUN-1998.
 05-DEC-1997; 97WO-US22125.
 06-DEC-1996; 96US-0033251.
 (MINU) UNIV MINNESOTA.
 Gahr PJ, Mitchell DT, Ohlendorf D, Schlievert PM;
 WPI; 1998-333329/29.
 Mutant non-lethal Streptococcus pyrogenic exotoxin type C - useful
 for vaccines to protect from biological activity of wild type toxin
 e.g. to prevent or ameliorate streptococcal toxic shock syndrome
 Claim 7; Page -: 55pp; English.
 The present sequence represents a mutant Streptococcus pyrogenic
 exotoxin type C (SPE-C) toxin. Streptococcus pyrogenes is a pathogen
 of humans which can cause mild infections e.g. impetigo or severe acute
 diseases SPE-C is thought to be associated with streptococcal toxic
 shock syndrome (STSS) and has several proposed biological activities,
 e.g. has been shown to block liver clearance of endotoxin and act
 as a "superantigen" i.e. induce T lymphocytes proliferation, resulting
 in abnormally high levels of circulating cytokines TNF- beta and
 IFN- gamma. The mutant toxins are useful in vaccines which can be
 administered to animals (especially humans) to protect against at
 least one biological activity of a wild-type SPE-C. Such vaccines are
 especially useful to reduce symptoms associated with toxic shock such
 as STSS in humans.
 note: this sequence does not appear in the specification; it was created
 using information provided.
 Sequence 235 AA;
 Query Match 24.6%; Score 297; DB 19; Length 235;
 Best Local Similarity 31.7%; Pred. No. 8e-19;
 Matches 76; Conservative 40; Mismatches 110; Indels 14; Gaps 5;
 QY 1 MKTKLIFSTSFIAISRPPVGLVDNNSLLRNI-----YSTIVYEYSDIVIDFKT 53
 DB 1 MKKNIKIIVITVILISTIS-PI--IKSDSKDISNVKSDLLAYATTIPYDKNCRVNFT 60
 QY 54 SHNLVTKKLDVRDARDFINSEMDYEAANDFKTGDKIAVFSVPDWNLSKGVYATYTG 113
 DB 61 THTLAIDTKYR-GKDYIISSEMSYASQKPKRDHVDVGL----FYILNSHTGYIYG 115
 QY 114 GITPYQKTSIPKPNVNLWNGKQISVPYNEISTNTTVAQEDLKVKKFLIAQHLYS 173
 DB 116 GITPAQNNKYNHKLGNLFISGESQQLNNKILIEKDIYVTFQEDFKIRKYLMDNKIYD 175
 QY 174 SSSYSKSGRLVHFHTNDNSKYSFDLF-YVGYRDKESIFKVKYDNKSNFIDKIGHLIEID 232
 DB 176 ATSPYVSGRIEIGTKDGKHE-QIDLFDPNENGRSDIFAKYKDNRIINMKNFHSFIDYLE 234

RESULT 5
 AAW62788
 ID AAW62788 standard; Protein; 235 AA.
 XX
 AC AAW62788;
 XX
 DT 24-SEP-1998 (first entry)
 XX
 DE Mutant streptococcal pyrogenic exotoxin type C (SPE-C).
 XX
 KW Streptococcus pyrogenic exotoxin type C; SPE-C toxin; STSS;
 KW streptococcal toxic shock syndrome; mutant; vaccine.
 XX
 OS Streptococcus pyrogenes.
 XX
 FT Key Location/Qualifiers
 FT Peptide 1..27
 FT Protein /note= "signal peptide"
 FT /note= "mature protein"
 FT /note= "mature protein"
 FT Misc-difference 44 optionally substituted with Ala"
 FT /label= Y17A
 FT /note= "Tyr at position 17 of the mature protein
 FT substituted with Ala"
 FT Misc-difference 65
 FT /label= N38A
 FT /note= "Asn at position 38 of the mature protein
 FT substituted with Ala"
 XX
 PN WO9824910-A2.
 XX
 PD 11-JUN-1998.
 XX
 PF 05-DEC-1997; 97WO-US22125.
 XX
 PR 06-DEC-1996; 96US-0033251.
 XX
 PA (MINU) UNIV MINNESOTA.
 XX
 PI Gahr PJ, Mitchell DT, Ohlendorf D, Schlievert PM;
 XX
 DR WPI; 1998-333329/29.
 XX
 PT Mutant non-lethal Streptococcus pyrogenic exotoxin type C - useful
 PT for vaccines to protect from biological activity of wild type toxin
 PT e.g. to prevent or ameliorate streptococcal toxic shock syndrome
 XX
 PS Claim 9; Page -: 55pp; English.
 XX
 CC The present sequence represents a mutant Streptococcus pyrogenic
 CC exotoxin type C (SPE-C) toxin. Streptococcus pyrogenes is a pathogen
 CC of humans which can cause mild infections e.g. impetigo or severe acute
 CC diseases SPE-C is thought to be associated with streptococcal toxic
 CC shock syndrome (STSS) and has several proposed biological activities,
 CC e.g. has been shown to block liver clearance of endotoxin and act
 CC as a "superantigen" i.e. induce T lymphocytes proliferation, resulting
 CC in abnormally high levels of circulating cytokines TNF- beta and
 CC IFN- gamma. The mutant toxins are useful in vaccines which can be
 CC administered to animals (especially humans) to protect against at
 CC least one biological activity of a wild-type SPE-C. Such vaccines are
 CC especially useful to reduce symptoms associated with toxic shock such
 CC as STSS in humans.
 CC note: this sequence does not appear in the specification; it was created
 CC using information provided.
 XX
 SQ Sequence 235 AA;
 Query Match 24.6%; Score 297; DB 19; Length 235;
 Best Local Similarity 31.7%; Pred. No. 8e-19;
 Matches 76; Conservative 41; Mismatches 109; Indels 14; Gaps 5;

QY 1 MKTKLIFSETSFIAIISRPVFGLEVDNNSLLRNISYIV-----YVSVDIVDFKT 53
 DB 1 MKKINIKIVFIITVILISTYFYHOSDSKDISNSKSDLLYAAITIPYDKDCRVNFS 60
 QY 54 SHNLVTKKLDVRDARDFINSEMDYAAANDFKTGDKIAVFSVPFDMNLSKGVATYTG 113
 DB 61 THTLAIDTQYR-GKDYVISSEMSYEASQFKRDRDHDVDFGL----FYILNSHTGEVIY 115
 QY 114 GITPYQKTSIPKNIPVNLINGKQISVPYNEISTNKTTVTAQETDLAVKRFELIAHQHLYS 173
 DB 116 GITPAQNNKVNHLKGLNLFISGESQQNLNKKIILEKIDIVTFOEIDFKIRKYLMDNYKIYD 175
 QY 174 SGSSYKSGRLVFHTNDNSDKYSFDLF-YVGYRDKESIFKVKONKSNIDKIGHLDIEID 232
 DB 176 ATSPYVSGRIEIGTKDGKHE-QIDLFDSPEGTRSDIFAKYKDNRIINMKNFSFDIYLE 234
 RESULT 6
 AAW62784
 ID AAW62784 standard; Protein; 235 AA.
 XX
 AC AAW62784;
 XX
 DT 24-SEP-1998 (first entry)
 XX
 DE Streptococcal pyrogenic exotoxin type C (SPE-C).
 XX
 KW Streptococcus pyrogenic exotoxin type C; SPE-C toxin; STSS;
 KW streptococcal toxic shock syndrome; mutant; vaccine.
 XX
 OS Streptococcus pyrogenes.
 XX
 FT Key Location/Qualifiers
 FT Peptide 1..27
 FT Protein /note= "signal peptide"
 FT /note= "mature protein"
 XX
 PN WO9824910-A2.
 XX
 PD 11-JUN-1998.
 XX
 PF 05-DEC-1997; 97WO-US22125.
 XX
 PR 06-DEC-1996; 96US-0033251.
 XX
 PA (MINU) UNIV MINNESOTA.
 XX
 PI Gahr PJ, Mitchell DT, Ohlendorf D, Schlievert PM;
 XX
 DR WPI; 1998-333329/29.
 DR N-PSDB; AAW42209.
 XX
 PT Mutant non-lethal Streptococcus pyrogenic exotoxin type C - useful
 PT for vaccines to protect from biological activity of wild type toxin
 PT e.g. to prevent or ameliorate streptococcal toxic shock syndrome
 XX
 PS Disclosure; Fig 1; 55pp; English.
 XX
 CC The present sequence represents a Streptococcus pyrogenic exotoxin type
 CC C (SPE-C) toxin. Streptococcus pyrogenes is a pathogen of humans which
 CC can cause mild infections e.g. impetigo or severe acute diseases e.g.
 CC scarlet fever and STSS. SPE-C is thought to be associated with
 CC streptococcal toxic shock syndrome (STSS) and has several proposed
 CC biological activities, e.g. has been shown to block liver clearance of
 CC endotoxin and act as a "superantigen" i.e. induce T lymphocytes
 CC proliferation, resulting in abnormally high levels of circulating
 CC cytokines TNF- beta and IFN- gamma. The SPE-C protein is mutated (see
 CC AAW62785-88) to make it substantially non-lethal compared to wild-type
 CC SPE-C toxin. The mutant toxins are useful in vaccines which can be
 CC administered to animals (especially humans) to protect against at least
 CC one biological activity of a wild-type SPE-C. Such vaccines are
 CC especially useful to reduce symptoms associated with toxic shock such as

Best Local Similarity 34.2%; Pred. No. 7.4e-18;
Matches 68; Conservative 35; Mismatches 85; Indels 11; Gaps 5;

QY 37 YSTIVVEYSDIVIDFKTSH--NLVTKKLDVRDARDFINSEMDEYAANDFTGDKIAVFS 94
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 17 YTITPYDYKCRVNFSHTLINDTQKY---RGKDYYISSEMSYEASOKFRDRDHVDVG 73

QY 95 VPFDDNYLSKGKVATAYTGGITPYPYOKTSIPKNIPVLNWLINGKQISTVPYNEISTNKTTVA 154
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 74 L-----FYILNSHTGEIYGGITPAQNKKVNHKLGLNFISGSQQONLNKIILEKDIPTF 129

QY 155 QEIDLKVKRFLIAOHOLYSSSGSYKSGRLVPHNTDNDSKYSPDLF-YVGYRDKEISIFKVY 213
||||||| : ||| : : ||| : | : | : | : | : | : | : | : | : | : |
Db 130 QEIDEKIRKYLMNDYKIYDAISPVSIGRIETGTDGKH-QIDLPDSPNEGTRSDIFAKY 188

QY 214 KDNKSFNIKIGHLDIEID 232
||| : | : || :
Db 189 KDNRIINKNFSSHFDIYLE 207

RESULT 8
AAR45018 ID AAR45018 standard; protein; 208 AA.
XX AC AAR45018;
XX DT 08-JUN-1994 (first entry)
XX DE Staphylococcal enterotoxin SPE C.
XX KW Staphylococcal enterotoxin; SE; cancer; tumouricidal agent;
XX KW autoimmune disease; toxicity; Protein A; perfusion system.
XX OS Staphylococcus aureus.
XX PN WO9324136-A.
XX PD 09-DEC-1993.
XX PF 01-JUN-1993; 93WO-US05213.
XX PR 01-JUN-1992; 92US-0891718.
XX PA (STON)/ STONE J L.
XX PI (TERM)/ TERMAN D S.
XX PI Stone JL, Terman DS;
XX DR WPI; 1993-405418/50.
XX PT Use of staphylococcal enterotoxin(s) and homologues - for
XX PT treating cancer in a patient or for the treatment of auto-immune
XX PT diseases
XX PS Disclosure; Fig 1; 90pp; English.

The sequences given in AAR45011-21 are Staphylococcal enterotoxins (SEs) which may be used in the methods of the invention for treating cancer in a patient. These SEs, and homologues of them, can be used as tumoricidal agents for treating cancers and autoimmune disease. They exhibit tumoricidal activity and toxicity identical to that observed for the Protein A perfusion system. They may be administered by i.v. injection.

XX Sequence 208 AA;
XX Query Match 23.7%; Score 285.5; DB 14; Length 208;
Best Local Similarity 34.2%; Pred. No. 7.4e-18;
Matches 68; Conservative 35; Mismatches 85; Indels 11; Gaps 5;

QY 37 YSTIVVEYSDIVIDFKTSH--NLVTKKLDVRDARDFINSEMDEYAANDFTGDKIAVFS 94
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 17 YTITPYDYKCRVNFSHTLINDTQKY---RGKDYYISSEMSYEASOKFRDRDHVDVG 73

[illegible]

DR N-PSDB; ABN69774.

XX New Streptococcus protein for the treatment or prevention of infection

PT or disease caused by Streptococcus bacteria, such as meningitis, and

PT for detecting a compound that binds to the protein -

XX Claim 1; Page 3891; 4525pp; English.

XX The invention relates to a protein (ABP25413-ABP30895) from group B

CC streptococcus/GBS (Streptococcus agalactiae) or group A streptococcus/GAS

CC (Streptococcus pyogenes), comprising one of 5483 sequences (SI), given in

CC the specification. The proteins have antibacterial and antiinflammatory

CC activity. (I), nucleic acids encoding (I), ABN66044-ABN71526 and

CC antibodies that bind (I) are used in the manufacture of medicaments for

CC the treatment or prevention of infection or disease caused by

CC Streptococcus bacteria, particularly S. agalactiae and S. pyogenes.

CC Nucleic acids encoding (I) are used to detect Streptococcus in a

CC biological sample. (I) is used to determine whether a compound binds to

CC (I). A composition comprising (I) or a nucleic acid encoding (I), may be

CC used as a vaccine or diagnostic composition. The disease caused by

CC Streptococcus that is prevented or treated may be meningitis. Nucleic

CC acid encoding (I) may be used to recombinantly produce (I) and may be

CC used in gene therapy. Antibodies to (I) are used for affinity

CC chromatography, immunoassays, and distinguishing/identifying

CC Streptococcus proteins.

XX Sequence . 232 AA;

Query Match 21.5%; Score 259; DB 23; Length 232;

Best Local Similarity 29.7%; Pred. No. 2.1e-15;

Matches 68; Conservative 41; Mismatches 102; Indels 18; Gaps 7;

QY 11 TSFIAIISRPVFGLEVDNNSL-----LRNIYSTIVYEYSDIVDFKTSNHLVTKKLDV 64

DB 7 TILVLIIFHGVSXKSDSENKDKVQLNAYEIIIPVDITNCNIDYLTTHDFY---IDI 63

QY 65 RD--ARDFFINSEMDYAAADFDTGDKIAVFSVPFDWNLVSKGKVTAYTYGGITP-YQKT 121

DB 64 SSVKKNFSDSEVESYITTKFKNKQVNIPLP-----YIFTRYDYVIYIGVTPSVNSN 119

QY 122 STPKNIPVNLWNGKQISVPYNEISTNKTVTVAQEDLKVRFELIAHQHLYSGSSYKSG 181

DB 120 SENSIVGNLLIDGVQOQTLNPIKIDKPIFTIQEFDKIRQVLMQTYKIYDNPSPYIKG 179

QY 182 RVEHFNDSKYSDFLF-YVGVRKESIFKYVKDKNSFNIDKIGHDI 229

DB 180 QLEIAINGKHE-SFNLIDATSSSTRSDIFKFKYDKNTINMKDFSHFDI 227

RESULT 14

AAU14103

XX AAU14103 standard; peptide; 257 AA.

XX AC AAU14103;

XX 21-NOV-2001 (first entry)

DE Peptide sequence from Staphylococcus aureus enterotoxin type E.

XX Anti-retroviral; DP178-like; DP107-like; enterotoxin type E;

KW antifusogenic; antiviral; HIV transmission.

XX Staphylococcus aureus.

OS WO200151673-A2.

PN 19-JUL-2001.

PD 05-JUL-2000; 2000WO-US35727.

PF 09-JUL-1999; 99US-0350841.

PR (TRIM-) TRIMERIS INC.

PA

XX Jeffs P, Lackey JW, Erickson JB, Lawless MK, Merutka G;

XX WPI; 2001-442157/47.

DR Identifying a compound that inhibits the formation of or disrupts a

XX DP107/DP178 complex, especially compounds with antifusogenic, antiviral

PT or intracellular modulatory activity, by detecting the formation of a

PT DP107/DP178 complex -

XX Disclosure; Flg 41; 259pp; English.

XX The present invention relates to peptides which exhibit anti-retroviral

CC activity. The peptides of the invention (AAU12559-AAU14009) comprise

CC DP178-like and DP107-like peptides. The DP178 peptide corresponds

CC to amino acids 639-673 of the transmembrane protein gp1 from human

CC immunodeficiency virus 1 (HIV-1) isolate LAI. The DP107 peptide

CC corresponds to amino acids 558-595 of gp41 from HIV-1LAI. The invention

CC also relates to a method of identifying compounds that inhibit the

CC formation of or disrupts a DP107/DP178 complex. The method comprises

CC detecting the formation of a DP107/DP178 complex, both in the presence

CC or absence of a test compound, in a reaction mixture containing DP107

CC and DP178 peptides. The method is useful for identifying compounds,

CC including small molecule compounds, which may themselves exhibit

CC antifusogenic, antiviral or intracellular modulatory activity. The

CC DP178-like/DP107-like peptides are useful to inhibit human and non-human

CC retroviral, particularly HIV, transmission to uninfected cells. The

CC present sequence represents a peptide sequence from Staphylococcus aureus

CC enterotoxin type E.

XX Sequence 257 AA;

Query Match 21.4%; Score 258.5; DB 22; Length 257;

Best Local Similarity 26.4%; Pred. No. 2.7e-15;

Matches 75; Conservative 55; Mismatches 67; Indels 87; Gaps 13;

QY 1 MKTKLIFSFTSIFIA--IISRPVFG-----LEVDNNSL--LRNIY--- 37

DB 1 MKTAFIL---LFIALTITSPLVNGSEKSEINEKDLKKSELOALNSLNLRQIYYN 57

QY 38 -----STIYVE-----YSDIVDFKTSNHLVTKKLDVDRDARDFIN 73

DB 58 EKAITENKESDDQFLENTLLFKGFTGHPWYNDLLVD-----LGSKDATNKYKG 106

QY 74 SEMDEYAANDFKTGDKIAVFSVPFDWNLVSKG---KVTAYTYGGITPYQKTSI--PKNIP 128

DB 107 KKYDLYGAY-----YGYOCAGGTPNKTACMYGGVTLHDNNRUTEKKVP 150

QY 129 VNLWNGKQISVPYNEISTNKTVTVAQEDLKVRFELIAHQHLYSS---GSSYKSGRLVF 185

DB 151 INLWIDGKQTVTFIDKVKTSKKEVTQVQELDQARHYLHGKFLGNSDSFGKVGQRLIVF 210

QY 186 HTNDSKYSDFLFYVGVRKESIFKYVKDKNSFNIDKIGHDI 229

DB 211 HSSEGS-TVSYDLFDAQOGQVPDITLLRIYRDNKTINSENH-HIDL 252

RESULT 15

AAU67339

ID AAB67339 standard; peptide; 230 AA.

XX AC AAB67339;

XX 23-APR-2001 (first entry)

DE Staphylococcus aureus enterotoxin E protein.

XX Tumour; cancer; immune; enterotoxin.

KW Staphylococcus aureus.

OS US6180097-B1.

PN

